Novel *Neisseria meningitidis* compounds and anti-infection applications thereof

FIELD OF THE INVENTION

This invention generally relates to novel *Neisseria meningitidis* (Nm) compounds, and to their anti-Nm infection applications. It more particularly relates to polynucleotides, herein referred to as Nm polynucleotide(s), polypeptides encoded by them (referred to herein as Nm polypeptide(s)), recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such Nm polypeptides and Nm polynucleotides in anti-Nm infection applications, such as diagnostic, prophylactic and therapeutic uses thereof including vaccines against Nm infections. In a further aspect, the invention relates to diagnostic assays for detecting an Nm infection.

BACKGROUND OF THE INVENTION

Neisseria meningitidis (meningococcus) is a Gram negative bacterium frequently isolated from the human upper respiratory tract. It occasionally causes invasive bacterial diseases such as bacteremia and meningitis. The incidence of meningococcal disease shows geographical seasonal and annual differences (Schwartz, B., Moore, P.S., Broome, C.V.; Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Most disease in temperate countries is due to strains of serogroup B, and varies in incidence from 1-10/100,000/year total population sometimes reaching higher values (Kaczmarski, E.B. (1997), Commun. Dis. Rep. Rev. 7: R55-9, 1995; Scholten, R.J.P.M., Bijlmer, H.A., Poolman, J.T. *et al.* Clin. Infect. Dis. 16: 237-246, 1993; Cruz, C., Pavez, G., Aguilar, E., *et al.* Epidemiol.

Infect. 105: 119-126, 1990).

Epidemics dominated by serogroup A meningococci, mostly in central Africa, are encountered, sometimes reaching levels up to 1000/100.000/year (Schwartz, B., Moore, P.S., Broome, C.V. Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Nearly all cases as a whole of meningococcal disease are caused by serogroup A, B, C, W-135 and Y meningococci and a tetravalent A, C, W-135, Y polysaccharide vaccine is available (Armand, J., Arminjon, F., Mynard, M.C., Lafaix, C., J. Biol. Stand. 10: 335-339, 1982).

The polysaccharide vaccines are currently being improved by way of chemical conjugating them to carrier proteins (Lieberman, J.M., Chiu, S.S., Wong, V.K., *et al.* JAMA 275 : 1499-1503, 1996).

A serogroup B vaccine is not available, since the B capsular polysaccharide was found to be nonimmunogenic, most likely because it shares structural similarity to host components (Wyle, F.A., Artenstein, M.S., Brandt, M.L. *et al.* J. Infect. Dis. 126: 514-522, 1972; Finne, J.M., Leinonen, M., Mäkelä, P.M. Lancet ii.: 355-357, 1983).

For many years efforts have been initiated and carried out to develop meningococcal outer membrane based vaccines (de Moraes, J.C., Perkins, B., Camargo, M.C. *et al.* Lancet 340: 1074-1078, 1992; Bjune, G., Hoiby, E.A. Gronnesby, J.K. *et al.* 338: 1093-1096, 1991). Such vaccines have demonstrated efficcacies from 57% - 85% in older children (>4 years) and adolescents, but none of them has demonstrated no significant efficacies in younger children/adults. These efficacies were further restricted to certain defined Nm strains, *i.e.* to the strain used to make the vaccine, and to related strains (*e.g.* of same electrophoretic type), without providing an efficient protection against most of the existing Nm

strains. Such vaccines does notably not provide an efficient protection against a wide range of Nm strains, such as every strain of at least one defined serogroup (such as serogroup B).

The frequency of *Neisseria meningitidis* infections has risen dramatically in the past few decades. This has been attributed to the emergence of multiply antibiotic resistant strains and an increasing population of people with weakened immune systems. It is no longer uncommon to isolate *Neisseria meningitidis* strains that are resistant to some or all of the standard antibiotics. This phenomenon has created an unmet medical need and demand for new anti-microbial agents, vaccines, drug screening methods, and diagnostic tests for this organism.

SUMMARY OF THE INVENTION

The present invention relates to *Neisseria meningitidis* (Nm) polynucleotides and polypeptides, recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such Nm polypeptides and polynucleotides, including prevention and treatment of Nm-related diseases. In a further aspect, the invention relates to diagnostic assays for detecting Nm-related diseases and conditions associated with Nm infections, such as assays for detecting expression or activity of Nm polynucleotides or polypeptides.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

DESCRIPTION OF THE INVENTION

The invention relates to *Neisseria meningitidis* (Nm) polypeptides and polynucleotides as described in greater detail below. In particular, the invention relates to Nm polynucleotides which cover the Nm genetic diversity and which correspond to Nm polypeptides of the outer membrane and/or the periplasma of Nm, and to the corresponding Nm polypeptide.

By "a polynucleotide which covers the Nm genetic diversity", it is herein meant that when assaying Nm Z2491, said polynucleotide can be observed as corresponding to at least an ORF fraction of more than 250 nucleotides, advantageously more than 500 nucleotides, preferably more than 750 nucleotides, but most preferably as corresponding to a complete ORF, and that said ORF is present in more than 70%, preferably in more than 80%, and more preferably in more than 90% of the strains of a panel of Nm strains chosen according to the MLST standard (multilocus sequence typing : see *e.g.* Maiden *et al.* 1998, Proc. Natl. Acad. Sci. 95 : 3140-3145) of which teaching is herein incorporated by reference. By "a polynucleotide corresponding to an ORF fraction, or a complete ORF" as above-mentioned, it is herein meant that said polynucleotide shows with said ORF fraction, or complete ORF, a sequence homology which is superior to about 85%, preferably to about 90%, more preferably to about 95%, and most preferably is a 100% homologue to said ORF fraction sequence, or ORF sequence. Such a panel may comprise Nm strains chosen serogroup A Nm strains, serogroup B Nm strains, serogroup C Nm strains, serogroup W135 Nm strains, and/or serogroup Y Nm strains. An advantageous Nm panel *e.g.* comprises Nm strains of the A, B, C, and W135 serogroups.

The invention relates especially to Nm compounds having the nucleotide and amino acid sequences set out in SEQ ID NO:1 to SEQ NO:90 (odd SEQ ID numbers for polynucleotides, even SEQ ID numbers for polypeptides), and are also illustrated in figures 1A to 45A (polynucleotides), and in figures 1B to 45B

(polypeptides). It is understood that sequences recited in the Sequence Listing below as "DNA" represent an exemplification of one embodiment of the invention, since those of ordinary skill will recognize that such sequences can be usefully employed in polynucleotides in general, including ribopolynucleotides.

Means for assaying the presence or absence of a polynucleotide in a bacterial strain are well known techniques to the person skilled in the art, and examples of such means comprise nucleic probe hybridization (see *e.g.* dot blot experiments in the below example 1). Said polynucleotide may correspond, or be part of a gene as well as, in certain Nm strains, to a pseudogene. Examples of such probes for said SEQ ID N°: 1-90 products include probes obtained by PCR amplification using the primers recited as SEQ ID N°: 97-116 and chromosomal DNA from Nm Z2491 as target DNA (see *e.g.* examples below and Table 2: SEQ ID N°97 and N°98 are nucleotidic forward and, respectively reverse primers for *dsb*A, SEQ ID N°99 and N°100 are nucleotidic forward and, respectively reverse primers for *fhu*A, SEQ ID N°101 and N°102 are nucleotidic forward and, respectively reverse primers for *rni*5, SEQ ID N°103 and N°104 are nucleotidic forward and, respectively reverse primers for *tol*C, SEQ ID N°105 and N°106 are nucleotidic forward and, respectively reverse primers for *rth*17, SEQ ID N°107 and N°108 are nucleotidic forward and, respectively reverse primers for *rth*18, SEQ ID N°109 and N°110 are nucleotidic forward and, respectively reverse primers for *rth*19, SEQ ID N°111 and N°112 are nucleotidic forward and, respectively reverse primers for *rth*20, SEQ ID N°113 and N°114 are nucleotidic forward and, respectively reverse primers for *rth*21, SEQ ID N°115 and N°116 are nucleotidic forward and, respectively reverse primers for *fha*B). Appropriate PCR conditions for obtaining such probes with said primers and DNA template can be determined by the person skilled in the art ; as an example, these conditions may be : 1 $\mu g.ml^{-1}$ of template DNA ; reaction buffer (10 mM Tris-Cl, pH 8.0, 50 mM KCl, 1.5 mM MgCl2, 0.001% gelatin) ; dATP, dCTP, dGTP and dTTP (200 µM each);

dimethylsulfoxide (5%); forward and reverse primers (100 nM each) and Taq polymerase ; PCR incubation: 1 min at 94°C, 30 cycles of 1 min at 94° C, 1.5 min at 5°C below the Tm of the oligonucleotide primers, and 2 min at 72° C followed by incubation for 5 min at 72° C.

It is understood that sequences recited herein as corresponding to any of SEQ ID N°:1-90 represent an exemplification of one embodiment of the invention since those of ordinary skill in the art will recognize that these sequences correspond to those identified on a panel of Nm strains constituted of Nm Z2491, Nm Z3524, Nm Z3842, Nm Z4667, Nm Z4707, Nm Z5005, Nm Z6466, Nm Z7176, Nm Z4662, Nm Z6904, Nm Z4259, Nm Z4673, Nm Z4683 (see "examples" below) as Nm ORF, and that variant, but homologue, *dsb*A, *fha*B, *fhu*A, *rni*5, *rth*17, *rth*18, *rth*19, *rth*20, *rth*21, *tol*C, sequences can be found in other Nm strains. Any appropriate technique can be implemented by the skilled person, *e.g.* sequencing the products which hibridize with said primers. Such variant sequences are thus encompassed by the present invention.

It is also understood that whereas the products of SEQ ID N°: 1-90 according to the invention are of first interest because of *inter alia* their Nm genetic diversity coverage, variant but homologue products which do not cover Nm genetic diversity on such a wide basis, can also be produced by the skilled person when desired. This means that the polypeptides and polynucleotides of the invention are candidates of first interest for construction or obtention of variant but homologue products which cover only one Nm serogroup, such as serogroup B, or which cover some but not all serogroups, such as serogroups B and A. Simple screening and/or trial and error tests can provide such variant sequences without undue burden. Such variant sequences are thus encompassed by the present invention.

Polypeptides

In one aspect of the invention there are provided polypeptides of *Neisseria meningitidis* referred to herein as Nm polypeptides as well as biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 ;

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91,over the entire length of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89 respectively;

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

The Nm polypeptide provided in SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 are the DsbA polypeptides from *Neisseria meningitidis* strains Z2491; Z3524, Z3842, Z4667, Z4707, Z5005, Z6466, Z7176, Z4662, Z6904, Z4259, Z4673, Z4683 respectively.

The Nm polypeptide provided in SEQ ID NO : 28 is the polypeptide (348 aminoacids) corresponding to the 3' end fraction of FhaB from *Neisseria meningitidis* strains Z2491.

The Nm polypeptides provided in SEQ ID NO : 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 are the FhuA polypeptides from *Neisseria meningitidis* strains Z2491, Z3524, Z3842, Z4259, Z4662; Z4667, Z4673, Z4683, Z4707, Z5005, Z6904, Z7176 respectively.

The Nm polypeptides provided in SEQ ID NO : 54 is the Rni5 polypeptide from *Neisseria meningitidis* strain Z2491.

The Nm polypeptides provided in SEQ ID NO : 56, 60, 62, 64 are the Rth17, respectively Rth18, Rth19, Rth20, Rth21 polypeptides from *Neisseria meningitidis* strain Z2491.

The Nm polypeptides provided in SEQ ID NO : 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 are the TolC polypeptides from *Neisseria meningitidis* strain Z2491, Z3524, Z4707, Z3842, Z4259, Z4662, Z4667, Z4673, Z4683, Z5005, Z6466, Z6904, Z7176 respectively.

The Nm polypeptides of which ORF has some correspondance (i.e. significant hit in a computer program for sequence identity determination such as a standard

BLAST program, see also the below "definitions" section), though with no significant sequence identity/similarly, with an previously described ORF in another bacteria species have been named according to this previously known ORF. This is particularly the case of DsbA, FhaB, FhuA, Rth17 and TolC (see the below "examples"). The Nm polypeptides of which ORF has no significant hit with any gene of known function have been named according to the region plus a sequential number. This is particularly the case of Rni5, Rth18, Rth19, Rth20, Rth21.

A source of said Nm strains is given in the below "examples".

The invention also provides an immunogenic fragment of a Nm polypeptide, that is, a contiguous portion of the Nm polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the Nm polypeptide. Such an immunogenic fragment may include, for example, the Nm polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

A fragment is a polypeptide having an amino acid sequence that is entirely the same as part but not all of any amino acid sequence of any polypeptide of the

invention. As with Nm polypeptides, fragments may be "free-standing," or comprised within a larger polypeptide of which they form a part or region, most preferably as a single continuous region in a single larger polypeptide.

Preferred fragments include, for example, truncation polypeptides having a portion of an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or of variants thereof, such as a continuous series of residues that includes an amino- and/or carboxyl-terminal amino acid sequence. Degradation forms of the polypeptides of the invention produced by or in a host cell, are also preferred. Further preferred are fragments characterized by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

Further preferred fragments include an isolated polypeptide comprising an amino acid sequence having at least 15, 20, 30, 40, 50 or 100 contiguous amino acids from the amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or an isolated polypeptide comprising an amino acid sequence having at least 15, 20, 30, 40, 50 or 100 contiguous amino acids truncated or deleted from the amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

Fragments of the polypeptides of the invention may be employed for producing

the corresponding full-length polypeptide by peptide synthesis; therefore, these fragments may be employed as intermediates for producing the full-length polypeptides of the invention.

Particularly preferred are variants in which several, 5-10, 1-5, 1-3, 1-2 or 1 amino acids are substituted, deleted, or added in any combination.

The polypeptides, or immunogenic fragments, of the invention may be in the form of the "mature" protein or may be a part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification such as multiple histidine residues, or an additional sequence for stability during recombinant production. Furthermore, addition of exogenous polypeptide or lipid tail or polynucleotide sequences to increase the immunogenic potential of the final molecule is also considered.

In one aspect, the invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa.

Furthermore, this invention relates to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates

to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. WO94/29458 and WO94/22914.

The proteins may be chemically conjugated, or expressed as recombinant fusion proteins allowing increased levels to be produced in an expression system as compared to non-fused protein. The fusion partner may assist in providing T helper epitopes (immunological fusion partner), preferably T helper epitopes recognised by humans, or assist in expressing the protein (expression enhancer) at higher yields than the native recombinant protein. Preferably the fusion partner will be both an immunological fusion partner and expression enhancing partner.

Fusion partners include protein D from *Haemophilus influenza*e and the non-structural protein from influenzae virus, NS1 (hemagglutinin). Another fusion partner is the protein known as LYTA. Preferably the C terminal portion of the molecule is used. Lyta is derived from *Streptococcus pneumoniae* which synthesize an N-acetyl-L-alanine amidase, amidase LYTA, (coded by the lytA gene {Gene, 43 (1986) page 265-272}) an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of E.coli C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at its amino terminus has been described {Biotechnology: 10, (1992) page 795-798}. It is possible to use the repeat portion of the Lyta molecule found in the C terminal end starting at residue 178, for example residues 188 - 305.

The present invention also includes variants of the aforementioned polypeptides, that is polypeptides that vary from the referents by conservative amino acid substitutions, whereby a residue is substituted by another with like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr; among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and Tyr.

Polypeptides of the present invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

Polynucleotides

It is an object of the invention to provide polynucleotides, herein designated Nm polynucleotides, which cover the Nm genetic diversity above and "examples" below for a definition of "Nm genetic diversity coverage"), and which correspond to outer membrane and/or periplasma Nm polypeptides. The present invention is particularly related to such Nm polynucleotides which comprises an ORF (open Reading Frame) coding for outer membrane and/or periplasma polypeptides.

In a particularly preferred embodiment of the invention the polynucleotide comprises a sequence set out in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or a variant thereof.

The Nm polynucleotides provided in SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 are the *dsb*A polynucleotides (complete ORF) from *Neisseria*

meningitidis strain Z2491, Z3524, Z3842, Z4667, Z4707, Z5055, Z6466, Z7176, Z4662, Z6904, Z4259, Z4673, Z4683 respectively.

The Nm polynucleotide provided in SEQ ID NO : 27 is the 3' end fraction (1047 nucleotides) of the *Fha*B ORF from *Neisseria meningitidis* strain Z2491.

The Nm polynucleotides provided in SEQ ID NO : 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 are the *fhu*A polynucleotides (complete ORF) from *Neisseria meningitidis* strain Z2491, Z3524, Z3842, Z4259, Z4662, Z4667, Z4673, Z4683, Z4707, Z5005, Z6904, Z7176 respectively.

The Nm polynucleotide provided in SEQ ID NO : 53 is the *rni*5 polynucleotide (complete ORF) from *Neisseria meningitidis* strain Z2491.

The Nm polynucleotides provided in SEQ ID NO : 55, 57, 59, 61, 63 are the *rth*17, respectively *rth*18, *rth*19, *rth*20, *rth*21 polynucleotides (complete ORF) from *Neisseria meningitidis* strain Z2491.

The Nm polynucleotides provided in SEQ ID NO : 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89 are the *tol*C polynucleotides (complete ORF) from *Neisseria meningitidis* strain Z2491, Z3524, Z4707, Z3842, Z4259, Z4662, Z4667, Z4673, Z4683, Z5005, Z6466, Z6904, Z7176 respectively.

As above explained for Nm polypeptides, Nm polynucleotides have been named according to the ORF with which some correspondance, though with no significant identity/similarity has been found in another species (*dsb*A, *fha*B, *fhuA*, *rth*17 and *tol*C), or, when no correspondance with a gene of known function has been found said Nm polynucleotides have been named according to the Nm region in which they have been located, plus a sequential number (*rni*5, *rth*18, *rth*19,

*rth*20, *rth*21).

As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing Nm polypeptides and polynucleotides, including, for example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a Nm polypeptide having a deduced amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, and polynucleotides closely related thereto and variants thereof.

In another particularly preferred embodiment of the invention there is a Nm polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, or a variant thereof.

Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, a polynucleotide of the invention encoding Nm polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing chromosomal DNA fragments from bacteria using *Neisseria*

meningitidis cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* (such as a lambda DashII library) or some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Examples of such probes can be obtained by PCR amplification with the primers SEQ ID N°: 97-116 and with Nm Z2491 DNA as target DNA (see example 1 and Table 2 below).

Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the polynucleotide sequence in both directions to determine a full length gene sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989) (see in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, was discovered in a DNA library derived from a *Neisseria meningitidis* panel (MLST).

Moreover, each DNA sequence set out in SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89 corresponds to an open reading frame (ORF) encoding a protein having about the number of amino acid residues set forth in SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, respectively with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art. The DNA sequence set out in SEQ ID N°: 27 corresponds to the 1047 3' end fraction of the ORF encoding a protein having about the number of amino acid residues set forth in SEQ ID NO: 28.

In a further aspect, the present invention provides for an isolated polynucleotide comprising or consisting of:

(a) a polynucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, over the entire length of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89,

(b) a polynucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 over the entire length of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26,

28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 respectively.

A polynucleotide encoding a polypeptide of the present invention may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide

can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA 86:* 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell 37:* 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding Nm polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 may be identical to the polypeptide encoding sequence contained in Nm nucleotides of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, respectively. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a *Neisseria meningitidis* polypeptide having an amino acid sequence set out in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization)

together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90. Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding Nm variants, that have the amino acid sequence of Nm polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, that do not alter the properties and activities of Nm polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 70% identical over their entire length to a polynucleotide encoding Nm polypeptide having an amino acid sequence set out in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, and polynucleotides that are complementary to such polynucleotides. Alternatively, most highly preferred are polynucleotides that comprise a region that is at least 80% identical over its entire length to a polynucleotide encoding Nm polypeptide and polynucleotides complementary thereto. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred,

and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to Nm polynucleotide sequences, such as those polynucleotides in SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x

SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein. Solution hybridization may also be used with the polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89 under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein. An appropriate library may e.g. be a lambda DashII library containing Nm Z2491 ADN fragments from about 12 to about 23 kb.

As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding Nm polypeptides, and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the Nm gene. Such probes generally will comprise at least 15 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs.

Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

A coding region of a Nm gene may be isolated by screening using a DNA sequence provided in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

There are several methods available and well known to those skilled in the art to obtain full-length DNAs, or extend short DNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman, *et al.*, *PNAS USA 85:* 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon™ technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon™ technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the DNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using "nested" primers, that is, primers designed to anneal within the amplified product (typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the selected gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length DNA constructed either by joining the product directly to the existing DNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the

design of the 5' primer.

The polynucleotides and polypeptides of the invention may be employed, for example, as research reagents and materials for discovery of treatments of and diagnostics for Nm-related diseases, particularly human Nm-related diseases, as further discussed herein relating to polynucleotide assays.

The polynucleotides of the invention that are oligonucleotides derived from a sequence of SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, may be used in the processes herein as described, but preferably for PCR, to determine whether or not the polynucleotides identified herein in whole or in part are transcribed in bacteria in infected tissue. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

The invention also provides polynucleotides that encode a polypeptide that is the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, may allow protein transport, may lengthen or shorten protein half-life or may facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in vivo*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

For each and every polynucleotide of the invention there is provided a polynucleotide complementary to it. It is preferred that these complementary

polynucleotides are fully complementary to each polynucleotide with which they are complementary.

A precursor protein, having a mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. When prosequences are removed such inactive precursors generally are activated. Some or all of the prosequences may be removed before activation. Generally, such precursors are called proproteins.

In addition to the standard A, G, C, T/U representations for nucleotides, the term "N" may also be used in describing certain polynucleotides of the invention. "N" means that any of the four DNA or RNA nucleotides may appear at such a designated position in the DNA or RNA sequence, except it is preferred that N is not a nucleic acid that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

In sum, a polynucleotide of the invention may encode a mature protein, a mature protein plus a leader sequence (which may be referred to as a preprotein), a precursor of a mature protein having one or more prosequences that are not the leader sequences of a preprotein, or a preproprotein, which is a precursor to a proprotein, having a leader sequence and one or more prosequences, which generally are removed during processing steps that produce active and mature forms of the polypeptide.

In accordance with an aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al., Hum Mol Genet* (1992) 1: 363, Manthorpe *et al., Hum. Gene Ther.* (1983) 4: 419), delivery of DNA complexed with specific protein carriers (Wu *et al., J Biol Chem.* (1989) 264: 16985), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, *PNAS USA*, (1986) 83: 9551), encapsulation of DNA in various forms of liposomes (Kaneda *et al., Science* (1989) 243: 375), particle bombardment (Tang *et al., Nature* (1992) 356:152, Eisenbraun *et al., DNA Cell Biol* (1993) 12: 791) and *in vivo* infection using cloned retroviral vectors (Seeger *et al., PNAS USA* (1984) 81: 5849).

Vectors, Host Cells, Expression Systems

The invention also relates to vectors that comprise a polynucleotide or polynucleotides of the invention, host cells that are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the invention.

Recombinant polypeptides of the present invention may be prepared by processes well known in those skilled in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems that comprise a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems, and to the production of polypeptides of

the invention by recombinant techniques.

For recombinant production of the polypeptides of the invention, host cells can be genetically engineered to incorporate expression systems or portions thereof or polynucleotides of the invention. Introduction of a polynucleotide into the host cell can be effected by methods described in many standard laboratory manuals, such as Davis, *et al.*, *BASIC METHODS IN MOLECULAR BIOLOGY*, (1986) and Sambrook, *et al.*, *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection.

Representative examples of appropriate hosts include bacterial cells, such as cells of streptococci, staphylococci, enterococci, *E. coli*, streptomyces, cyanobacteria, *Bacillus subtilis*, and *Neisseria meningitidis*; fungal cells, such as cells of a yeast, *Kluveromyces*, *Saccharomyces*, a basidiomycete, *Candida albicans* and *Aspergillus*; insect cells such as cells of *Drosophila* S2 and *Spodoptera* Sf9; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293, CV-1 and Bowes melanoma cells; and plant cells, such as cells of a gymnosperm or angiosperm.

A great variety of expression systems can be used to produce the polypeptides of the invention. Such vectors include, among others, chromosomal-, episomal- and virus-derived vectors, for example, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses, picornaviruses, retroviruses, and alphaviruses and vectors derived from combinations thereof, such as those derived from plasmid and

bacteriophage genetic elements, such as cosmids and phagemids. The expression system constructs may contain control regions that regulate as well as engender expression. Generally, any system or vector suitable to maintain, propagate or express polynucleotides and/or to express a polypeptide in a host may be used for expression in this regard. The appropriate DNA sequence may be inserted into the expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, (*supra*).

In recombinant expression systems in eukaryotes, for secretion of a translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, ion metal affinity chromatography (IMAC) is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and or purification.

The expression system may also be a recombinant live microorganism, such as a virus or bacterium. The gene of interest can be inserted into the genome of a live recombinant virus or bacterium. Inoculation and *in vivo* infection with this live vector will lead to *in vivo* expression of the antigen and induction of

immune responses. Viruses and bacteria used for this purpose are for instance: poxviruses (*e.g.* vaccinia, fowlpox, canarypox), alphaviruses (Sindbis virus, Semliki Forest Virus, Venezuelian Equine Encephalitis Virus), adenoviruses, adeno-associated virus, picornaviruses (poliovirus, rhinovirus), herpesviruses (varicella zoster virus, *etc.*), Listeria, Salmonella , Shigella, BCG. These viruses and bacteria can be virulent, or attenuated in various ways in order to obtain live vaccines. Such live vaccines also form part of the invention.

Diagnostic, Prognostic, Serotyping and Mutation Assays

This invention is also related to the use of Nm polynucleotides and Nm polypeptides of the invention for use as diagnostic reagents. Detection of Nm polynucleotides and/or polypeptides in an eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of Nm-related disease, staging of disease or response of an infectious organism to drugs. Eukaryotes, particularly mammals, and especially humans, particularly those infected or suspected to be infected with an organism comprising the Nm gene or protein, may be detected at the nucleic acid or amino acid level by a variety of well known techniques as well as by methods provided herein.

Polypeptides and polynucleotides for prognosis, diagnosis or other analysis may be obtained from a putatively infected and/or infected individual's bodily materials. Polynucleotides from any of these sources, particularly DNA or RNA, may be used directly for detection or may be amplified enzymatically by using PCR or any other amplification technique prior to analysis. RNA, particularly mRNA, cDNA and genomic DNA may also be used in the same ways. Using amplification, characterization of the species and strain of infectious or resident organism present in an individual, may be made by an analysis of the genotype of a selected polynucleotide of the organism. Deletions and insertions can be

detected by a change in size of the amplified product in comparison to a genotype of a reference sequence selected from a related organism, preferably a different species of the same genus or a different strain of the same species. Point mutations can be identified by hybridizing amplified DNA to labeled Nm polynucleotide sequences. Perfectly or significantly matched sequences can be distinguished from imperfectly or more significantly mismatched duplexes by DNase or RNase digestion, for DNA or RNA respectively, or by detecting differences in melting temperatures or renaturation kinetics. Polynucleotide sequence differences may also be detected by alterations in the electrophoretic mobility of polynucleotide fragments in gels as compared to a reference sequence. This may be carried out with or without denaturing agents. Polynucleotide differences may also be detected by direct DNA or RNA sequencing. See, for example, Myers *et al.*, *Science, 230:* 1242 (1985). Sequence changes at specific locations also may be revealed by nuclease protection assays, such as RNase, V1 and S1 protection assay or a chemical cleavage method. See, for example, Cotton *et al.*, *Proc. Natl. Acad. Sci., USA, 85:* 4397-4401 (1985).

In another embodiment, an array of oligonucleotides probes comprising Nm nucleotide sequence or fragments thereof can be constructed to conduct efficient screening of, for example, genetic mutations, serotype, taxonomic classification or identification. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability (see, for example, Chee *et al.*, *Science, 274: 610* (1996)).

Thus in another aspect, the present invention relates to a diagnostic kit which comprises:

(a) at least one polynucleotide of the present invention, preferably the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23,

25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or a fragment thereof ; and/or

(b) at least one nucleotide sequence complementary to that of (a); and/or

(c) at least one polypeptide of the present invention, preferably the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or a fragment thereof; and/or

(d) at least one antibody to a polypeptide of the present invention, preferably to the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a Nm-related disease.

This invention also relates to the use of polynucleotides of the present invention as diagnostic reagents. Detection of a mutated form of a polynucleotide of the invention, preferably, SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, which is associated with a Nm-related disease or pathogenicity will provide a diagnostic tool that can add to, or define, a diagnosis of said disease, a prognosis of a course of disease, a determination of a stage of disease, or a susceptibility to said disease, which results from under-expression, over-expression or altered expression of the polynucleotide. Organisms, particularly infectious organisms, carrying mutations in such polynucleotide may be detected at the polynucleotide level by a variety of techniques, such as those described elsewhere herein.

Cells from an organism carrying mutations or polymorphisms (allelic variations) in a polynucleotide and/or polypeptide of the invention may also be detected at the polynucleotide or polypeptide level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations in the RNA. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA, cDNA or genomic DNA may also be used for the same purpose, PCR. As an example, PCR primers complementary to a polynucleotide encoding Nm polypeptide can be used to identify and analyze mutations.

The invention further provides primers with 1, 2, 3 or 4 nucleotides removed from the 5' and/or the 3' end. These primers may be used for, among other things, amplifying Nm DNA and/or RNA isolated from a sample derived from an individual, such as a bodily material. The primers may be used to amplify a polynucleotide isolated from an Nm-infected individual, such that the polynucleotide may then be subject to various techniques for elucidation of the polynucleotide sequence. In this way, mutations in the polynucleotide sequence may be detected and used to diagnose and/or prognose the infection or its stage or course, or to serotype and/or classify the infectious agent.

The invention further provides a process for diagnosing infections caused by *Neisseria meningitidis*, comprising determining from a sample derived from an individual, such as a bodily material, an increased level of expression of polynucleotide having a sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89. Increased or decreased expression of a Nm polynucleotide can be measured using any on of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern

blotting, spectrometry and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-expression of Nm polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a Nm polypeptide, in a sample derived from a host, such as a bodily material, are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis, antibody sandwich assays, antibody detection and ELISA assays.

The polynucleotides of the invention may be used as components of polynucleotide arrays, preferably high density arrays or grids. These high density arrays are particularly useful for diagnostic and prognostic purposes. For example, a set of spots each comprising a different gene, and further comprising a polynucleotide or polynucleotides of the invention, may be used for probing, such as using hybridization or nucleic acid amplification, using a probes obtained or derived from a bodily sample, to determine the presence of a particular polynucleotide sequence or related sequence in an individual. Such a presence may indicate the presence of a pathogen, particularly *Neisseria meningitidis*, and may be useful in diagnosing and/or prognosing a Nm-related infection or a course of infection. A grid comprising a number of variants of the polynucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, are preferred. Also preferred is a comprising a number of variants of a polynucleotide sequence encoding the polypeptide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90.

Antibodies

The polypeptides and polynucleotides of the invention or variants thereof, or cells expressing the same can be used as immunogens to produce antibodies immunospecific for such polypeptides or polynucleotides respectively.

In certain preferred embodiments of the invention there are provided antibodies against Nm polypeptides or polynucleotides.

Antibodies generated against the polypeptides or polynucleotides of the invention can be obtained by administering the polypeptides and/or polynucleotides of the invention, or epitope-bearing fragments of either or both, analogues of either or both, or cells expressing either or both, to an animal, preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Köhler, G. and Milstein, C., *Nature 256:* 495-497 (1975); Kozbor *et al.*, *Immunology Today 4:* 72 (1983); Cole *et al.*, pg. 77-96 in *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc. (1985).

Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to polypeptides or polynucleotides of this invention. Also, transgenic mice, or other organisms or animals, such as other mammals, may be used to express humanized antibodies immunospecific to the polypeptides or polynucleotides of the invention. preferably, said antibodies can bind to atleast one Nm polypeptide according to the invention in *in vivo* conditions, or in *in vitro* ones mimicking *in vivo* ones, but do not recognize the patient cells.

Alternatively, phage display technology may be utilized to select antibody genes with binding activities towards a polypeptide of the invention either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Nm or from naive libraries (McCafferty, *et al.*, (1990), Nature 348, 552-554; Marks, *et al.*, (1992) *Biotechnology 10*, 779-783). The affinity of these antibodies can also be improved by, for example, chain shuffling (Clackson *et al.*, (1991) *Nature 352:* 628).

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptides or polynucleotides of the invention to purify the polypeptides or polynucleotides by, for example, affinity chromatography.

Thus, among others, antibodies against Nm-polypeptide or Nm-polynucleotide may be employed to treat infections, particularly bacterial infections.

Polypeptide variants include antigenically, epitopically or immunologically equivalent variants form a particular aspect of this invention.

Preferably, the antibody or variant thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized," where the complimentarity determining region or regions of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones *et al.* (1986), *Nature* 321, 522-525 or Tempest *et al.*, (1991) *Biotechnology* 9, 266-273.

Antagonists and Agonists - Assays and Molecules

Polypeptides and polynucleotides of the invention may also be used to assess the

binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology 1(2):* Chapter 5 (1991).

The screening methods may simply measure the binding of a candidate compound to the polypeptide or polynucleotide, or to cells or membranes bearing the polypeptide or polynucleotide, or a fusion protein of the polypeptide by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve competition with a labeled competitor. Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide or polynucleotide, using detection systems appropriate to the cells comprising the polypeptide or polynucleotide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Constitutively active polypeptide and/or constitutively expressed polypeptides and polynucleotides may be employed in screening methods for inverse agonists or inhibitors, in the absence of an agonist or inhibitor, by testing whether the candidate compound results in inhibition of activation of the polypeptide or polynucleotide, as the case may be. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide or polynucleotide of the present invention, to form a mixture, measuring Nm polypeptide and/or polynucleotide activity in the mixture, and comparing the Nm polypeptide and/or polynucleotide activity of the mixture to a standard. Fusion proteins, such as those made from Fc portion and Nm polypeptide, as hereinbefore described, can also be used for high-throughput screening assays

to identify antagonists of the polypeptide of the present invention, as well as of phylogenetically and/or functionally related polypeptides (see D. Bennett *et al.*, J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies that bind to and/or interact with a polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and/or polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents which may inhibit or enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of Nm polypeptides or polynucleotides, particularly those compounds that are bacteristatic and/or bactericidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising Nm polypeptide and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be a Nm agonist or antagonist. The ability of the candidate molecule to agonize or antagonize the Nm polypeptide is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of Nm polypeptide are most likely to be good antagonists. Molecules that bind well and, as the case may be, increase the rate of product production from

substrate, increase signal transduction, or increase chemical channel activity are agonists. Detection of the rate or level of, as the case may be, production of product from substrate, signal transduction, or chemical channel activity may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric, labeled substrate converted into product, a reporter gene that is responsive to changes in Nm polynucleotide or polypeptide activity, and binding assays known in the art.

Another example of an assay for Nm agonists is a competitive assay that combines an Nm compound according to the invention and a potential agonist with Nm compound binding molecules, recombinant Nm binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. Said Nm compound can be labeled, such as by radioactivity or a colorimetric compound, such that the number of Nm molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include, among others, small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide and/or polypeptide of the invention and thereby inhibit or extinguish its activity or expression. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a binding molecule, without inducing activities induced by a Nm compound according to the invention, thereby preventing the action or expression of Nm polypeptides and/or polynucleotides by excluding Nm polypeptides and/or polynucleotides from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding

molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem. 56:* 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of NMEN.

In a further aspect, the present invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa. Furthermore, this invention relates to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. WO94/29458 and WO94/22914.

Each of the polynucleotide sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the polynucleotide sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct

antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide, agonist or antagonist of the invention to interfere with the initial physical interaction between a pathogen or pathogens and a eukaryotic, preferably mammalian, host responsible for sequelae of infection. In particular, the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive and/or gram negative bacteria, to eukaryotic, preferably mammalian, extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block bacterial adhesion between eukaryotic, preferably mammalian, extracellular matrix proteins and bacterial Nm proteins that mediate tissue damage and/or; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

In accordance with yet another aspect of the invention, there are provided Nm agonists and antagonists of said Nm compounds according to the invention, preferably bacteristatic or bactericidal agonists and antagonists.

The antagonists and agonists of the invention may be employed, for instance, to prevent, inhibit and/or treat Nm-related diseases.

In a further aspect, the present invention relates to mimotopes of the polypeptide of the invention. A mimotope is a peptide sequence, sufficiently similar to the native peptide (sequentially or structurally), which is capable of being recognised by antibodies which recognise the native peptide; or is capable of raising antibodies which recognise the native peptide when coupled to a suitable carrier.

Peptide mimotopes may be designed for a particular purpose by addition, deletion or substitution of elected amino acids. Thus, the peptides may be modified for the purposes of ease of conjugation to a protein carrier. For example, it may be desirable for some chemical conjugation methods to include a terminal cysteine. In addition it may be desirable for peptides conjugated to a protein carrier to include a hydrophobic terminus distal from the conjugated terminus of the peptide, such that the free unconjugated end of the peptide remains associated with the surface of the carrier protein. Thereby presenting the peptide in a conformation which most closely resembles that of the peptide as found in the context of the whole native molecule. For example, the peptides may be altered to have an N-terminal cysteine and a C-terminal hydrophobic amidated tail. Alternatively, the addition or substitution of a D-stereoisomer form of one or more of the amino acids may be performed to create a beneficial derivative, for example to enhance stability of the peptide.

Alternatively, peptide mimotopes may be identified using antibodies which are capable themselves of binding to the polypeptides of the present invention using techniques such as phage display technology (EP 0 552 267 B1). This technique, generates a large number of peptide sequences which mimic the structure of the native peptides and are, therefore, capable of binding to anti-native peptide antibodies, but may not necessarily themselves share significant sequence homology to the native polypeptide.

Vaccines

Another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, preferably humans, which comprises inoculating the individual with Nm polynucleotide

and/or Nm polypeptide, or a fragment or variant thereof, adequate to produce antibody and/ or T cell immune response to protect said individual from infection, particularly bacterial infection and most particularly *Neisseria meningitidis* infection. Also provided are methods whereby such immunological response slows bacterial replication. Yet another aspect of the invention relates to a method of inducing immunological response in an individual which comprises delivering to such individual a nucleic acid vector, sequence or ribozyme to direct expression of Nm polynucleotide and/or polypeptide, or a fragment or a variant thereof, for expressing Nm polynucleotide and/or polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response, such as, to produce antibody and/ or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said individual, preferably a human, from a Nm-related disease, whether that disease is already established within the individual or not. One example of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a ribozyme, a modified nucleic acid, a DNA/RNA hybrid, a DNA-protein complex or an RNA-protein complex. The expression system may also be a recombinant live micro-organism, such as a virus or a bacterium, which can be virulent, or attenuated in various ways in order to obtain live vaccines (see "Vectors, Host Cells, Expression Systems" above).

A further aspect of the invention relates to an immunological composition that when introduced into an individual, preferably a human, capable of having induced within it an immunological response, induces an immunological response in such individual to a Nm polynucleotide and/or Nm polypeptide encoded therefrom, wherein the composition comprises a recombinant Nm polynucleotide and/or polypeptide encoded therefrom and/or comprises DNA and/or RNA which encodes and expresses an antigen of said Nm

polynucleotide, polypeptide encoded therefrom, or other polypeptide of the invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity and/or cellular immunity, such as cellular immunity arising from CTL or CD4+ T cells.

The immunological methods and compositions according to the invention advantageously show efficacies against at least one Nm strain belonging to one serogroup, preferably against at least two Nm strains belonging to more than one Nm serogroups, preferably more than two Nm serogroups, most preferably more than three Nm serogroups *e.g.* against Nm serogroups A, B, C and W135 and/or Y.

A Nm polypeptide or a fragment thereof may be fused with co-protein or chemical moiety which may or may not by itself produce antibodies, but which is capable of stabilizing the first protein and producing a fused or modified protein which will have antigenic and/or immunogenic properties, and preferably protective properties. Thus fused recombinant protein, preferably further comprises an antigenic co-protein, such as lipoprotein D from *Haemophilus influenzae*, Glutathione-S-transferase (GST) or beta-galactosidase, or any other relatively large co-protein which solubilizes the protein and facilitates production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system of the organism receiving the protein. The co-protein may be attached to either the amino- or carboxy-terminus of the first protein.

Provided by this invention are compositions, particularly vaccine compositions, and methods comprising the polypeptides and/or polynucleotides of the invention and immunostimulatory DNA sequences, such as those described in Sato, Y. *et al.* Science 273: 352 (1996).

Also, provided by this invention are methods using the described polynucleotide or particular fragments thereof, which have been shown to encode non-variable regions of bacterial cell surface proteins, in polynucleotide constructs used in such genetic immunization experiments in animal models of infection with *Neisseria meningitidis*. Such experiments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. It is believed that this approach will allow for the subsequent preparation of monoclonal antibodies of particular value, derived from the requisite organ of the animal successfully resisting or clearing infection, for the development of prophylactic agents or therapeutic treatments of bacterial infection, particularly *Neisseria meningitidis* infection, in mammals, particularly humans.

The invention also includes a vaccine formulation which comprises an immunogenic recombinant polypeptide and/or polynucleotide of the invention together with a suitable carrier, such as a pharmaceutically acceptable carrier. The vaccine formulation according to the invention advantageously shows efficacies against at least one Nm serogroup, advantageously more than 2 Nm serogroups, preferably more than 3 Nm serogroups (*e.g.* Nm serogroups A, B, C and W135 and/or Y), most preferably against any Nm strain.

Since the polypeptides and polynucleotides may be broken down in the stomach, each is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, or intradermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteristatic compounds and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or

thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. Preferably, the vaccine formulation according to the invention is a anti-Nm meningitidis formulation.

The vaccine formulation of the invention may also include adjuvant systems for enhancing the immunogenicity of the formulation. Preferably the adjuvant system raises preferentially a TH1 type of response.

An immune response may be broadly distinguished into two extreme catagories, being a humoral or cell mediated immune responses (traditionally characterised by antibody and cellular effector mechanisms of protection respectively). These categories of response have been termed TH1-type responses (cell-mediated response), and TH2-type immune responses (humoral response).

Extreme TH1-type immune responses may be characterised by the generation of antigen specific, haplotype restricted cytotoxic T lymphocytes, and natural killer cell responses. In mice TH1-type responses are often characterised by the generation of antibodies of the IgG2a subtype, whilst in the human these correspond to IgG1 type antibodies. TH2-type immune responses are characterised by the generation of a broad range of immunoglobulin isotypes including in mice IgG1, IgA, and IgM.

It can be considered that the driving force behind the development of these two types of immune responses are cytokines. High levels of TH1-type cytokines tend to favour the induction of cell mediated immune responses to the given antigen, whilst high levels of TH2-type cytokines tend to favour the induction

of humoral immune responses to the antigen.

The distinction of TH1 and TH2-type immune responses is not absolute. In reality an individual will support an immune response which is described as being predominantly TH1 or predominantly TH2. However, it is often convenient to consider the families of cytokines in terms of that described in murine CD4 +ve T cell clones by Mosmann and Coffman (*Mosmann, T.R. and Coffman, R.L. (1989) TH1 and TH2 cells: different patterns of lymphokine secretion lead to different functional properties. Annual Review of Immunology, 7, p145-173*). Traditionally, TH1-type responses are associated with the production of the INF-γ and IL-2 cytokines by T-lymphocytes. Other cytokines often directly associated with the induction of TH1-type immune responses are not produced by T-cells, such as IL-12. In contrast, TH2- type responses are associated with the secretion of IL-4, IL-5, IL-6 and IL-13.

It is known that certain vaccine adjuvants are particularly suited to the stimulation of either TH1 or TH2 - type cytokine responses. Traditionally the best indicators of the TH1:TH2 balance of the immune response after a vaccination or infection includes direct measurement of the production of TH1 or TH2 cytokines by T lymphocytes *in vitro* after restimulation with antigen, and/or the measurement of the IgG1:IgG2a ratio of antigen specific antibody responses.

Thus, a TH1-type adjuvant is one which preferentially stimulates isolated T-cell populations to produce high levels of TH1-type cytokines when re-stimulated with antigen *in vitro*, and promotes development of both CD8+ cytotoxic T lymphocytes and antigen specific immunoglobulin responses associated with TH1-type isotype.

Adjuvants which are capable of preferential stimulation of the TH1 cell response are described in International Patent Application No. WO 94/00153 and WO 95/17209.

3 De-O-acylated monophosphoryl lipid A (3D-MPL) is one such adjuvant. This is known from GB 2220211 (Ribi). Chemically it is a mixture of 3 De-O-acylated monophosphoryl lipid A with 4, 5 or 6 acylated chains and is manufactured by Ribi Immunochem, Montana. A preferred form of 3 De-O-acylated monophosphoryl lipid A is disclosed in European Patent 0 689 454 B1 (SmithKline Beecham Biologicals SA).

Preferably, the particles of 3D-MPL are small enough to be sterile filtered through a 0.22micron membrane (European Patent number 0 689 454).
3D-MPL will be present in the range of 10mg - 100mg preferably 25-50mg per dose wherein the antigen will typically be present in a range 2-50mg per dose.

Another preferred adjuvant comprises QS21, an Hplc purified non-toxic fraction derived from the bark of Quillaja Saponaria Molina. Optionally this may be admixed with 3 De-O-acylated monophosphoryl lipid A (3D-MPL), optionally together with an carrier.

The method of production of QS21 is disclosed in US patent No. 5,057,540.

Non-reactogenic adjuvant formulations containing QS21 have been described previously (WO 96/33739). Such formulations comprising QS21 and cholesterol have been shown to be successful TH1 stimulating adjuvants when formulated together with an antigen.

Further adjuvants which are preferential stimulators of TH1 cell response

include immunomodulatory oligonucleotides, for example unmethylated CpG sequences as disclosed in WO 96/02555.

Combinations of different TH1 stimulating adjuvants, such as those mentioned hereinabove, are also contemplated as providing an adjuvant which is a preferential stimulator of TH1 cell response. For example, QS21 can be formulated together with 3D-MPL. The ratio of QS21 : 3D-MPL will typically be in the order of 1 : 10 to 10 : 1; preferably 1:5 to 5 : 1 and often substantially 1 : 1. The preferred range for optimal synergy is 2.5 : 1 to 1 : 1 3D-MPL: QS21.

Preferably a carrier is also present in the vaccine composition according to the invention. The carrier may be an oil in water emulsion, or an aluminium salt, such as aluminium phosphate or aluminium hydroxide.

A preferred oil-in-water emulsion comprises a metabolisible oil, such as squalene, alpha tocopherol and Tween 80. In a particularly preferred aspect the antigens in the vaccine composition according to the invention are combined with QS21 and 3D-MPL in such an emulsion. Additionally the oil in water emulsion may contain span 85 and/or lecithin and/or tricaprylin.

Typically for human administration QS21 and 3D-MPL will be present in a vaccine in the range of 1mg - 200mg, such as 10-100mg, preferably 10mg - 50mg per dose. Typically the oil in water will comprise from 2 to 10% squalene, from 2 to 10% alpha tocopherol and from 0.3 to 3% tween 80. Preferably the ratio of squalene: alpha tocopherol is equal to or less than 1 as this provides a more stable emulsion. Span 85 may also be present at a level of 1%. In some cases it may be advantageous that the vaccines of the present invention will further contain a stabiliser.

Non-toxic oil in water emulsions preferably contain a non-toxic oil, e.g. squalane or squalene, an emulsifier, e.g. Tween 80, in an aqueous carrier. The aqueous carrier may be, for example, phosphate buffered saline.

A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil in water emulsion is described in WO 95/17210.

The present invention also provides a polyvalent vaccine composition comprising a vaccine formulation of the invention in combination with other antigens, in particular antigens useful for treating cancers, or autoimmune diseases. Such a polyvalent vaccine composition may include a TH-1 inducing adjuvant as hereinbefore described.

While the invention has been described with reference to certain Nm polypeptides and polynucleotides, it is to be understood that this covers fragments of the naturally occurring polypeptides and polynucleotides, and similar polypeptides and polynucleotides with additions, deletions or substitutions which do not substantially affect the immunogenic properties of the recombinant polypeptides or polynucleotides.

Compositions, kits and administration

In a further aspect of the invention there are provided compositions comprising a Nm polynucleotide and/or a Nm polypeptide for administration to a cell or to a multicellular organism.

The invention also relates to compositions comprising a polynucleotide and/or a polypeptides discussed herein or their agonists or antagonists. The polypeptides

and polynucleotides of the invention may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to an individual. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a polypeptide and/or polynucleotide of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration. The invention further relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention.

Polypeptides, polynucleotides and other compounds of the invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

In a further aspect, the present invention provides for pharmaceutical compositions comprising a therapeutically effective amount of a polypeptide and/or polynucleotide, such as the soluble form of a polypeptide and/or polynucleotide of the present invention, agonist or antagonist peptide or small molecule compound,

in combination with a pharmaceutically acceptable carrier or excipient. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. Polypeptides, polynucleotides and other compounds of the present invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds. The present invention also provides for a therapeutic composition useful in treating animals or humans with *Neisseria meningitidis*-related disease, said composition comprising at least one antibody directed against a polypeptide according to the invention, and a suitable pharmaceutical carrier. Preferably, said antibody does not recognize the patient cells.

The composition will be adapted to the route of administration, for instance by a systemic or an oral route. Preferred forms of systemic administration include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or intraperitoneal, can be used. Alternative means for systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if a polypeptide or other compounds of the present invention can be formulated in an enteric or an encapsulated formulation, oral administration may also be possible. Administration of these compounds may also be topical and/or localized, in the form of salves, pastes, gels, solutions, powders and the like.

For administration to mammals, and particularly humans, it is expected that the daily dosage level of the active agent will be from 0.01 μg/kg to 100 μg/kg, preferably from 0.1 to 10 μg/kg, typically around 1 μg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual and will vary with the age, weight and response of the particular

individual. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

The dosage range required depends on the choice of peptide, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages, however, are in the range of 0.1-100 μg/kg of subject.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.5-5 microgram/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks. With the indicated dose range, no adverse toxicological effects will be observed with the compounds of the invention which would preclude their administration to suitable individuals. A preferred vaccine composition is an anti-Nm meningitidis vaccine composition.

Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration by intravenous injection. Variations in these dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

Sequence Databases, Sequences in a Tangible Medium, and Algorithms

Polynucleotide and polypeptide sequences form a valuable information resource with which to determine their 2- and 3-dimensional structures as well as to

identify further sequences of similar homology. These approaches are most easily facilitated by storing the sequence in a computer readable medium and then using the stored data in a known macromolecular structure program or to search a sequence database using well known searching tools, such as the GCG program package.

Also provided by the invention are methods for the analysis of character sequences or strings, particularly genetic sequences or encoded protein sequences. Preferred methods of sequence analysis include, for example, methods of sequence homology analysis, such as identity and similarity analysis, DNA, RNA and protein structure analysis, sequence assembly, cladistic analysis, sequence motif analysis, open reading frame determination, nucleic acid base calling, codon usage analysis, nucleic acid base trimming, and sequencing chromatogram peak analysis.

A computer based method is provided for performing homology identification. This method comprises the steps of: providing a first polynucleotide sequence comprising the sequence of a polynucleotide of the invention in a computer readable medium; and comparing said first polynucleotide sequence to at least one second polynucleotide or polypeptide sequence to identify homology.

A computer based method is also provided for performing homology identification, said method comprising the steps of: providing a first polypeptide sequence comprising the sequence of a polypeptide of the invention in a computer readable medium; and comparing said first polypeptide sequence to at least one second polynucleotide or polypeptide sequence to identify homology.

All publications and references, including but not limited to patents and patent

applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

DEFINITIONS

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as the case may be, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heine, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM *J. Applied Math., 48:* 1073 (1988). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available computer programs. Computer program methods to determine identity between two sequences include, but are not limited to, the GAP program in the GCG program package (Devereux, J., et al., *Nucleic Acids Research 12(1):* 387 (1984)), BLASTP, BLASTN (Altschul, S.F. et al., *J. Molec. Biol. 215:* 403-410 (1990), and FASTA(Pearson and Lipman Proc. Natl. Acad. Sci. USA 85; 2444-2448 (1988). The BLAST family of programs is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., *et al.*, NCBI NLM NIH Bethesda, MD 20894; Altschul, S., *et al., J. Mol. Biol. 215*: 403-410 (1990). The well known Smith Waterman algorithm may also be used to determine identity.

Parameters for polypeptide sequence comparison include the following:
Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)
Comparison matrix: BLOSSUM62 from Henikoff and Henikoff,
Proc. Natl. Acad. Sci. USA. 89:10915-10919 (1992)
Gap Penalty: 8
Gap Length Penalty: 2
A program useful with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison WI. The aforementioned parameters are the default parameters for peptide comparisons (along with no penalty for end gaps).

Parameters for polynucleotide comparison include the following:
Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)
Comparison matrix: matches = +10, mismatch = 0
Gap Penalty: 50
Gap Length Penalty: 3
Available as: The "gap" program from Genetics Computer Group, Madison WI. These are the default parameters for nucleic acid comparisons.

A preferred meaning for "identity" for polynucleotides and polypeptides, as the case may be, are provided in (1) and (2) below.

(1) Polynucleotide embodiments further include an isolated polynucleotide comprising a polynucleotide sequence having at least a 70, 80, 85, 90, 95, 97 or 100% identity to the reference sequence of SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, wherein said polynucleotide sequence may be identical to the reference sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37,

39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or may include up to a certain integer number of nucleotide alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence, and wherein said number of nucleotide alterations is determined by multiplying the total number of nucleotides in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of nucleotides in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89:

$$n_n \leq x_n - (x_n \bullet y),$$

wherein n_n is the number of nucleotide alterations, x_n is the total number of nucleotides in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, y is 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and $\bullet$ is the symbol for the multiplication operator, and wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting it from x_n. Alterations of a polynucleotide sequence encoding the polypeptide of SEQ ID

NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

By way of example, a polynucleotide sequence of the present invention may be identical to the reference sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, that is it may be 100% identical, or it may include up to a certain integer number of nucleic acid alterations as compared to the reference sequence such that the percent identity is less than 100% identity. Such alterations are selected from the group consisting of at least one nucleic acid deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleic acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of nucleic acid alterations for a given percent identity is determined by multiplying the total number of nucleic acids in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of nucleic acids in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or :

$$n_n \leq x_n - (x_n \circ y),$$

wherein n_n is the number of nucleic acid alterations, x_n is the total number of nucleic acids in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., • is the symbol for the multiplication operator, and wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting it from x_n.

(2) Polypeptide embodiments further include an isolated polypeptide comprising a polypeptide having at least a 70, 77, 80, 87, 89 or 100% identity to a polypeptide reference sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, wherein said polypeptide sequence may be identical to the reference sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or may include up to a certain integer number of amino acid alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence, and wherein said number of amino acid alterations is determined by multiplying the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88,

or 90, by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 :

$$n_a \leq x_a - (x_a \circ y),$$

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, y is 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and $\circ$ is the symbol for the multiplication operator, and wherein any non-integer product of x_a and y is rounded down to the nearest integer prior to subtracting it from x_a.

By way of example, a polypeptide sequence of the present invention may be identical to the reference sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, that is it may be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the percent identity is less than 100% identity. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference

sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 :

$$n_a \leq x_a - (x_a \circ y),$$

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and $\circ$ is the symbol for the multiplication operator, and wherein any non-integer product of x_a and y is rounded down to the nearest integer prior to subtracting it from x_a.

"Individual(s)," when used herein with reference to an organism, means a multicellular eukaryote, including, but not limited to a metazoan, a mammal, an ovid, a bovid, a simian, a primate, and a human.

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated

from the coexisting materials of its natural state is "isolated", as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is "isolated" even if it is still present in said organism, which organism may be living or non-living.

"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA including single and double-stranded regions.

"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Disease(s)" means any disease caused by or related to infection by at least one *Neisseria meningitidis* strain, such as Nm meningitis.

In the below examples, reference is made to figures 1 to 50 which represent (for fig. 1 to 45: "A" letters for polynucleotidic sequences, "B" letters for polypeptidic ones) :

- figures 1 to 13 correspond *dsb*A/DsBA sequences obtained :
  - for allele 1 :
    - from Nm strain Z2491 (Fig. 1A, 1B),
    - from Nm strain Z3524 (Fig. 2A, 2B),
    - from Nm strain Z3842 (Fig. 3A, 3B),
    - from Nm strain Z4667 (Fig. 4A, 4B),
    - from Nm strain Z4707 (Fig. 5A, 5B),
    - from Nm strain Z5005 (Fig. 6A, 6B),
    - from Nm strain Z6466 (Fig. 7A, 7B),
    - from Nm strain Z7176 (Fig. 8A, 8B),
  - for allele 2 :
    - from Nm strain Z4662 (Fig. 9A, 9B),
    - from Nm strain Z6904 (Fig. 10A, 10B),
  - for allele 3 :
    - from Nm strain Z4259 (Fig. 11A, 11B),
    - from Nm strain Z4673 (Fig. 12A, 12B),
  - for allele 4:
    - from Nm strain Z4683 (Fig. 13A, 13B),

- figures 14A (1047 nucleotides) et 14B (348 aminoacids) correspond to the 3' end fraction of the *fha*B, respectively FhaB, sequences obtained from Nm strain Z2491,

- figures 15 to 26 correspond to *fhu*A, FhuA sequences obtained from :
  - from Nm strain Z2491 (Fig. 15A, 15B),
  - from Nm strain Z3524 (Fig. 16A, 16B),
  - from Nm strain Z3842 (Fig. 17A, 17B),

- from Nm strain Z4259 (Fig. 18A, 18B),
- from Nm strain Z4662 (Fig. 19A, 19B),
- from Nm strain Z4667 (Fig. 20A, 20B),
- from Nm strain Z4673 (Fig. 21A, 21B),
- from Nm strain Z4683 (Fig. 22A, 22B),
- from Nm strain Z4707 (Fig. 23A, 234B),
- from Nm strain Z5005 (Fig. 24A, 24B),
- from Nm strain Z6904 (Fig. 25A, 25B),
- from Nm strain Z7176 (Fig. 26A, 26B),

- figures 27A et 27B correspond to *rni*5, respectively Rni5, sequences obtained from Nm Z2491,

- figures 28A et 28B correspond to *rth17*, respectively Rth17, sequences obtained from Nm Z2491,

- figures 29A et 29B correspond to *rth*18, respectively Rth18, sequences obtained from Nm Z2491,

- figures 30A et 30B correspond to *rth*19, respectively Rth19, sequences obtained from Nm Z2491,

- figures 31A et 31B correspond to *rth*20, respectively Rth20, sequences obtained from Nm Z2491,

- figures 32A et 32B correspond to *rth*21, respectively Rth21, sequences obtained from Nm Z2491,

- figures 33 to 45 correspond to *tol*C/TolC sequences obtained :
  - for allele 1 :
    - from Nm strain Z2491 (Fig. 33A, 33B),
    - from Nm strain Z3524 (Fig. 34A, 34B),
  - for allele 2 :
    - from Nm strain Z4707 (Fig. 35A, 35B),
  - for allele 3 :
    - from Nm strain Z3842 (Fig. 36A, 36B),

- from Nm strain Z4259 (Fig. 37A, 37B),
- from Nm strain Z4662 (Fig. 38A, 38B),
- from Nm strain Z4683 (Fig. 39A, 39B),
- from Nm strain Z4673 (Fig. 40A, 40B),
- from Nm strain Z4667 (Fig.41A, 41B),
- from Nm strain Z5005 (Fig. 42A, 42B),
- from Nm strain Z6466 (Fig. 43A, 43B),
- from Nm strain Z6904 (Fig. 44A, 44B),
- from Nm strain Z7176 (Fig. 45A, 45B),

- figure 46 illustrates the production of a knockout mutation of DsbA,

- figures 47A and 47B illustrate the immunofluorescence microscopy performed on wild-type ans DsbA mutant bacteria with anti-recombinat DsbA antiserum (fig. 47A: wild type Nm 8013 ; fig. 47B: DsbA mutant 8013),

- figure 48 illustrates the bactericidal activity of anti-DsbA and the corresponding pre-immune serum

- figure 49 illustrates the bactericidal activity of anti-DsbA antiserum against meningococci expressing an isogenic mutant lacking the protein DsbA,

- figure 50 illustrates Northern blot controls of the presence of DsbA in every MLST strains.

EXAMPLE 1 :

The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. The examples are illustrative, but do not limit the invention.

Strains of Nm were tested that represent the genetic diversity of this species according to MLST (Maiden *et al.* 1998, *supra*). .

Table 1

Nm strain Z number	Serological group	Clonal subgroup	ST
2491	A	IV-1	4
5005	A	I	1
3524	A	III	5
6466	A	IX	60
4662	B	groupe A4	8
3842	B	ET-5 (44/76)	32
7176	B	ET-5 (MC58)	74
4673	B	Lignée 3	41
4259	C	ET-37 (FAM18)	11
6904	W135	ET-37 (ROU)	11
4690	B	Autre	25
4683	B	Autre	30
4707	B	Autre	49
4667	B	Autre	48

Their MLST assignments were : ST1 (subgroup I, strain B40); ST2 (subgroup VI, Z6835); ST4 (subgroup IV-1, Z2491 (Sarkari *et al.*, 1994 Mol. Microbiol. 13 : 207-217)), ST5 (subgroup III, Z3524); ST8 (A4 cluster, BZ 10); ST11 (ET-37 complex, serogroup C: FAM18 ; serogroup W135: ROU (Pron *et al.*, 1997, J.

Infect. Dis. 176 : 1285-1292)); ST 25 (NG G40); ST30 (NG 4/88); ST32 (ET-5 complex, 44/76); ST41 (lineage 3, BZ 198); ST48 (BZ147); ST49 (297-0); ST60q (subgroup IX, 890592) et ST74 (ET-5 complex, MC58 (Virji *et al.*, 1995, Mol. Microbiol. 18 : 741-754)).

Nm were grown on GC agar (GCB, Difco), with the addition of Kellogg's defined supplement plus ferric nitrate (Kellog *et al.*, 1963) for 12 to 20 hours at 37°C in a moist atmosphere containing 5% CO_2. Liquid media were GC-PO_4 (1.5 % Protease peptone number3 (Difco), 0.5 % NaCl, 30 mM potassium phosphate, pH 7.5) and GC-Hepes (like GC-PO_4 but potassium phosphate replaced by 30 mM Hepes, pH7.5) both supplemented as for the solid medium.

- Cloning of the polynucleotides coding for outer membrane and/or periplasma polypeptides in each Nm strains

By sequencing a Nm DNA library, such as a lambda DashII library containing 12-23 kb DNA fragments of Nm Z2491, nine ORF coding for outer membrane and/or periplasma polypeptides were cloned into *E. coli* and sequenced:

- *dsb*A (allele 1) SEQ ID N°: 1 (corresponding polypeptide: SEQ ID N°: 2),
- *fhu*A SEQ ID N°: 29 (corresponding polypeptide: SEQ ID N°: 30),
- *rni*5 SEQ ID N°: 53 (corresponding polypeptide: SEQ ID N°: 54),
- *rth*17 SEQ ID N°: 55 (corresponding polypeptide: SEQ ID N°: 56),
- *rth*18 SEQ ID N°: 57 (corresponding polypeptide: SEQ ID N°: 58),
- *rth*19 SEQ ID N°: 59 (corresponding polypeptide: SEQ ID N°: 60),
- *rth*20 SEQ ID N°: 61 (corresponding polypeptide: SEQ ID N°: 62),
- *rth*21 SEQ ID N°: 63 (corresponding polypeptide: SEQ ID N°: 64),
- *tol*C (allele 1) SEQ ID N°: 65 (corresponding polypeptide: SEQ ID N°: 66).

A further tenth ORF was identified as *fha*B, but only a 3' end fraction of this ORF is herewith given:SEQ ID N° 27 (1047 nucleotides).

These sequences are illustrated by figures 1A and 1B, 14A and 14B, 27A and 27B, 28A and 28B, 29A and 29B, 30A and 30B, 31A and 31B, 32A and 32B, 33A and 33B, respectively, as above-recited (fig. number + A letter: polynucleotides ; same fig. number + B letter: corresponding polypeptides).

From these 10 new products isolated from Nm Z2491, probes were constructed so as to determine whether these 9 new ORF and the complete ORF corresponding to said new *fha*B ORF fraction are also present in the MLST Nm panel. Means for obtaining such probes include PCR amplification using the primers recited as SEQ ID N°: 97-116 and chromosomal DNA from Nm Z2491 as target DNA. Appropriate PCR conditions for obtaining such probes with said primers and DNA template can be determined by the person skilled in the art ; as an example, these conditions may be : 1 $\mu g.ml^{-1}$ of template DNA ; reaction buffer (10 mM Tris-Cl, pH 8.0, 50 mM KCl, 1.5 mM MgCl2, 0.001% gelatin) ; dATP, dCTP, dGTP and dTTP (200 µM each); dimethylsulfoxide (5%); forward and reverse primers (100 nM each) and Taq polymerase ; PCR incubation: 1 min at 94°C, 30 cycles of 1 min at 94° C, 1.5 min at 5°C below the Tm of the oligonucleotide primers, and 2 min at 72° C followed by incubation for 5 min at 72° C. Primer sequences are given in the below Table 2, together with the size of the PCR products thus obtained:

Table 2

ORF	forward primer	5'-3' sequence	reverse primer	5'-3' sequence	size of PCR product (kb)
fhaB (probe, N-term)	fhaB-for	AAAGCACAGCACCATGGTTGCAGTAG CCGAAAC (SEQ ID N°115)	fhaB-rev	AGTGTCTTTAGCCTCAATTACAGCAGCA CTGCC (SEQ ID N°116)	1.40
*rth*17	rth17-for	ACCGTGAGGCGGACTTGGC (SEQ ID N°107)	rth17-rev	TGGCCCGCATTGTCGGGTTTAAAGCCGT CTTCG (SEQ ID N°108)	0.32
*rth*18 *	rth18-for	ATTTGCGGAGGGCGAACTGG (SEQ ID N°109)	rth18-rev	GCTTCGCAAAAGCCGACTTG (SEQ ID N°110)	0.40
*rth*19	rth19-for	GGCAACCGATTGCCATCATC (SEQ ID N°111)	rth19-rev	TTTCCGTTTTCAGACGGCTG (SEQ ID N°112)	0.27
*rth*20	rth20-for	AAGACCGTAAAAATGCAGGCG (SEQ ID N°113)	rth20-rev	TTTCCGACTTTGCGGGAGTG (SEQ ID N°114)	0.29
*rth*21	rth21-for	GGTTGGCTGCTTTCAAACGC (SEQ ID N°115)	rth21-rev	ATTAAATATTTTGTCCGCTTGTAC (SEQ ID N°116)	0.28

* primers for *rth18* are lying upstream of the start and downstream of the stop codon.

ORF	forward primer	5'-3' sequence	reverse primer	5'-3' sequence	size of PCR product (kb)
tolC	tolC-for	GCCTGACACTGACGCCCTATTTGCA ACATGAAC (SEQ ID N°103)	tolC-rev	TACCGTGCTTGAGCCAGTTCTGTTCTGC TTGG (SEQ ID N°104)	1.28
dsbA	dsbA-for	GCTTTGACTTCATTGACCCTGTTGG CATTGGCC (SEQ ID N°97)	dsbA-rev	TATCCACCAACTGGTCAATCGTGGTCATA CCGG (SEQ ID N°99)	0.65
fhuA	fhuA-for	CCACGCTGATTATTGCTTCCTTCCC TGTTGCTG (SEQ ID N°99)	fhuA-rev	ACCCGGCATAGAGTCCGAACGCCAATATT TTTG (SEQ ID N°100)	2.04
rni5	rni5-for	TGTTTCCCACCCAAACTTAC (SEQ ID N°101)	rni5-rev	GTTCGTGGATGCAGACATAG (SEQ ID N°102)	0.36

These hybridization experiments performed under usual stringency conditions led to the conclusion that the nine new ORF and the complete ORF corresponding to the new fhaB fraction, which were isolated from Nm Z2491, are present in every Nm strain of the MLST panel. DNA dot blot hybridization was performed according to the DIG System Users Guide (Boehringer). One microliter containing 100 ng of denatured chromosomal DNA from each strain was spotted on nylon membranes (Hybond N, Amersham) and hybridized with DIG-labeled probes obtained by PCR amplification of each ORF. The hybridizations were performed using high SDS buffer (Church buffer) at 37° C, and the last washing step was with 0.5 x SSC, 0.1% SDS at 50° C in order to allow approximately 30% mismatch. Positive hybridization signals were detected by chemiluminescence.

Some of these precise sequences corresponding to those initially isolated in Nm Z2491 are shown on (A letter for polynucleotides; B letter for corresponding polypeptides):

- fig. 2A and 2B (Nm Z3524 ; SEQ ID N°3 and 4, respectively), fig. 3A and 3B (Nm Z4832 ; SEQ ID N°5 and 6, respectively), fig. 4A and 4B (Nm Z4667 ; SEQ ID N°7 and 8, respectively), fig. 5A and 5B (Nm Z4707 ; SEQ ID N°9 and 10, respectively), fig. 6A and 6B (Nm Z5005 ; SEQ ID N°11 and 12, respectively), fig. 7A and 7B (Nm Z6466 ; SEQ ID N°13 and 14, respectively), fig. 8A and 8B (Nm Z7176 ; SEQ ID N°15 and 16, respectively), fig. 9A and 9B (Nm Z4662 ; SEQ ID N°17 and 18, respectively), fig. 10A and 10B (Nm Z6904 ; SEQ ID N°19 and 20, respectively), fig. 11A and 11B (Nm Z4259 ; SEQ ID N°21 and 22, respectively), fig. 12A and 12B (Nm Z4673 ; SEQ ID N°23 and 24, respectively), fig. 13A and 13B (Nm Z4683 ; SEQ ID N°25 and 26, respectively), for *dsb*A (respectively DsbA),

- fig. 16A and 16B (Nm Z3524 ; SEQ ID N°31 and 32, respectively), fig. 17A and 17B (Nm Z3842 ; SEQ ID N°33 and 34, respectively), fig. 18A and 18B

(Nm Z4259 ; SEQ ID N°35 and 36, respectively), fig. 19A and 19B (Nm Z4662 ; SEQ ID N°37 and 38, respectively), fig. 20A and 20B (Nm Z4667 ; SEQ ID N°39 and 40, respectively), fig. 21A and 21B (Nm Z4673 ; SEQ ID N°41 and 42, respectively), fig. 22A and 22B (Nm Z4683 ; SEQ ID N°43 and 44, respectively), fig. 23A and 23B (Nm Z4707 ; SEQ ID N°45 and 46, respectively), fig. 24A and 24B (Nm Z5005 ; SEQ ID N°47 and 48, respectively), fig. 25A and 25B (Nm Z6904 ; SEQ ID N°49 and 50, respectively), fig. 26A and 26B (Nm Z7176 ; SEQ ID N°51 and 52, respectively), for *fhu*A (respectively FhuA),

- fig. 34A and 34B (Nm Z3524 ; SEQ ID N°67 and 68, respectively), fig. 35A and 35B (Nm Z4707 ; SEQ ID N°69 and 70, respectively), fig. 36A and 36B (Nm Z3842 ; SEQ ID N°71 and 72, respectively), fig. 37A and 37B (Nm Z4259 ; SEQ ID N°73 and 74, respectively), fig. 38A and 38B (Nm Z4662 ; SEQ ID N°75 and 76, respectively), fig. 39A and 39B (Nm Z4683 ; SEQ ID N°77 and 78, respectively), fig. 40A and 40B (Nm Z4673 ; SEQ ID N°79 and 80, respectively), fig. 41A and 41B (Nm Z4667 ; SEQ ID N°81 and 82, respectively), fig. 42A and 42B (Nm Z5005 ; SEQ ID N°83 and 84, respectively), fig. 43A and 43B (Nm Z6466 ; SEQ ID N°85 and 86, respectively), fig. 44A and 44B (Nm Z6904 ; SEQ ID N°87 and 88, respectively), fig. 45A and 45B (Nm Z7176 ; SEQ ID N°89 and 90, respectively), for *tol*C (respectively TolC).

Below is illustrated the high identity % observed for each of these compounds when comparing different Nm strains tested.

Table 3

Identity (%) between the *fhu*A DNA sequences (5 alleles) of the different Nm strains tested.

Only intact gene sequences have been compared (no pseudogenes)

	Z4683	Z4259	Z6904	Z7176
Z2491	97,2	96,9	96,2	98,7
Z4683		96,5	96,1	98,2
Z4259			98,9	98,0
Z6904				97,0

Table 4

Identity/similarly (%) between the FhuA proteins of the different Nm strains tested.

	Z4683	Z4259	Z6904	Z7176
Z2491	98,0 / 98,1	97,6 / 97,9	97,0 / 97,4	99,6
Z4683		96,7 / 97,2	96,9 / 97,2	98,4 / 98,6
Z4259			99,1 / 99,3	98,0 / 98,3
Z6904				97,4 / 97,9

Table 5

Identity (%) between the dsbA DNA sequences (4 alleles) of the different Nm strains tested.

	Z4662	Z4259	Z4683
Z2491	99,9	97,7	98,0
Z4662		97,6	97,8
Z4259			99,7

Nm strains which are below reported as linked by an "=" sign show an identical *dsb*A sequence.

Z2491=Z3524=Z3842=Z4667=Z4707=Z5005=Z6466=Z7176

Z4662=Z6904

Z4259=Z4673

Z4683

Table 6

Identity similarly (%) between the DsbA proteins (3 types) of the different Nm strains tested.

	Z4259	**Z4683**
Z2491	99,8 / 98,3	98,3 / 98,7
Z4259		99,6

Nm strains which are below reported as linked by an "=" sign show an identical *dsb*A sequence.

Z2491=Z3524=Z3842=Z4667=Z4707=Z5005=Z6466=Z7176=Z4662=Z6904

Z4259=Z4673

Z4683

Table 7

Identity (%) between the *tol*C DNA sequences (4 alleles) of the different Nm strains tested.

	Z4259	**Z4683**	**Z4707**
Z2491	99,8	99,7	99,9
Z4259		99,9	99,6
Z4683			99,6

Nm strains which are below reported as linked by an "=" sign show an identical *dsb*A sequence

Z2491=Z3524

Z4259==Z6904=Z3842=Z7176=Z6466=Z5005=Z4673=Z4667=Z4662

Z4683

Z4707 (pseudogene with a 4 pb deletion, which causes a stop codon after 16aa)

Identity / similarly between the TolC proteins (2 types) of the different NM strains tested.

Nm strains which are below reported as linked by an "=" sign show an identical *dsb*A sequence

Z2491 compared to Z4259 : identity = similarly = 99,8 %

Z2491=Z3524

Z4259=Z6904=Z3842=Z7176=Z6466=Z5005=Z4673=Z4667=Z4662=Z4683

The 45 polynucleotides herein illustrated thus appear as covering the Nm genetic diversity, as assessed by said MLST standard test. The person skilled in the art can further verify this Nm genetic diversity coverage by standard polynucleotide detection tests (*e.g.* with the help of said SEQ ID N°: 97-116 primers) performed in any other statistically significant Nm panel, and observe that said Nm polynucleotides are present in more than 90%, preferably more than 95%, more preferably in 100% of the Nm panel.

Each of said 45 Nm polynucleotides (ORF) were assessed for homologies to known proteins using standard BLAST programs as described in the below "definitions" section.

These results are illustrated in the below table 8.

Table 8. Open reading frames common to all Nm strains tested, and their correspondance (BLAST hits) with known proteins

		Known protein					
ORF	length (aa)	function	species	length (aa)	P	%identity / %similarity	Accession #
fhaB	2015	filamentous hemagglutinin B precursor	B. pertussis	3591	1e-50	25/42	P12255
rth17	181	gene 25	phage SPP1	271	4e-04	28/39	X97918
ORFs with no significant hit (length in aa) rth18 (78), rth19 (155), rth20 (101), rth21 (115)							
tolC	467	outer membrane protein	E. coli	495	5e-20	23/40	P02930
fhuA	703	ferrichrome iron receptor	E. coli	747	5e-26	23/40	P06971
dsbA	231	disulfide oxidoreductase	P. syringae	214	3e-18	28/47	AF036929
rni5	230	MTH939, unknown function	Methanobacterium	188	1e-7	27/47	AE000868

The products according to the invention thus appear as novel compounds.

EXAMPLE 2 : Efficacy of the products according to the invention such as DsbA (SEQ ID N°2) from *Neisseria meningitdis* for the production of anti-meningococcal vaccines

In order to be considered as a good vaccine candidate against endemic meningococcal infections, a purified protein has to induce protective antibodies against a wide range of strains representative of the meningococcal population. Subsequently, to be considered as a vaccine candidate a protein has to be immunogenic, to be expressed on the outer membrane, and to induce protective antibodies. In this example (i) we demonstrate that DsbA is expressed in a set of NM strains representative of the meningococcal population by northern blots, (ii) we purified the protein and raised antibodies in rabbit, (iii) using this polyclonal antibody and immunofluorescence of whole bacteria we localised the protein on the outermembrane, (iv) we engineered a non polar mutation and using this mutant we demonstrate that the anti DsbA polyclonal antibody has a bactericidal activity against the wild type strain and not against the isogenic mutant. In this example, DsbA (SEQ ID N°2) was purified as a recombinant protein lacking the signal sequence associated with a hexahistidine tract only in order to facilitate purification. The same procedure can be implemented by the skilled person with any preparation of DsbA isolated directly from *Neisseria meningitidis*, by immunological or biochemical means and all other recombinant forms of the protein, or similarly with any product according to the invention.

I. Northern Blot

Controls of the presence of said recombinant DsbA in every MLST Nm strain have been performed by Northern blot analysis, as below detailed. These controls have confirmed

said DsbA covers Nm genetic diversity, as *e.g.* illustrated by figure 50 (Northern blots lanes are given in the below table 9). The marker used was the RNA molecular weight marker I, digoxigenin-labeled, from Boehringer, with 9 fragments, the sizes are indicated in the blot.

Bacteria

Table 9:

lane	strain
1	Nm, serogroup A, subgroup IV-1
2	Nm, serogroup A, subgroup III
3	Nm, serogroup A, subgroup I
4	Nm, serogroup A, subgroup VI
5	Nm, serogroup A, subgroup IX
6	Nm, serogroup C, ET-37 complex, FAM18
7	Nm, serogroup W135, ET-37 complex, ROU
8	Nm, serogroup B, ET-5 complex, 44/76
9	Nm, serogroup B, ET-5 complex, MC58
10	Nm, serogroup B, Lineage 3
11	Nm, serogroup B, A4 cluster
12	Nm, serogroup B, ST25
13	Nm, serogroup B, ST30
14	Nm, serogroup B, ST48
15	Nm, serogroup B, ST49
16	Ng, FA1090

The *Neisseria meningitidis* strains chosen for RNA analysis represent the genetic diversity of this species according to multilocus sequence typing (MLST) (Maiden *et al.*, 1998).

Isolation of total RNA from *Neisseria*

Bacteria were grown on supplemented GC plates overnight at 37°C, 5% CO_2, 95% humidity. Single colonies were inoculated in 5 ml supplemented GC medium and grown at 37°C, 180 rpm until an optical density of Klett 50 was reached. 4 ml bacterial culture was pelleted by centrifugation (5000 rpm, 10 min).

RNA isolation was performed using the RNAqueous Kit (Ambion, Austin, TX, USA) according to the manufacturer's protocol: The bacterial pellet was resuspended in 350 µl Lysis/Binding Solution. 400 µl 64% ethanol were added and mixed by repeated pipetting. 400 µl of the lysate/ethanol mixture were applied to a filter cartridge and centrifuged in a microcentrifuge for 1 min. The flow-through was discarded and the remaining lysate/ethanol mixture was centrifuged through the filter. The filter cartridge was once washed with 700 µl Wash Solution #1 and twice with 500 µl Wash Solution #2/3. The wash solutions were passed through the filter by centrifugation for 1 min; the last traces of wash solution were removed by 2 min centrifugation after the last washing step. The filter cartridge was transferred to a fresh collection tube and 60 µl of elution solution was added to the center of the filter. The cartridge was incubated in a heat block at 65°C for 10 min and the eluate was recovered by centrifugation for 1 min. This elution step was repeated with another 60 µl of elution solution. The concentration of the RNA was measured in a 1:10 dilution in elution solution. The average RNA yield was around 1.5 µg/µl. RNA was stored at -80°C.

RNA electrophoresis and transfer (Northern blot)

A 1% denaturing agarose gel was prepared by dissolving 0.5 g agarose in 40.5 ml H_2O and cooling to 60°C. 5 ml 10 x MOPS buffer (0.2 M MOPS, pH 7.0, 0.05 M sodium-acetate, 0.01 M EDTA) and 4.5 ml formaldehyde (37%) were added and the gel was poured (gel size: 13 cm x 7.5 cm). 1 x MOPS was used as running buffer.

The RNA samples (ca. 3 µg per lane) were mixed with 4 volumes of gel loading solution

(supplied with the RNAqueous Kit) containing 10 µg/ml ethidium bromide. The samples were heated at 65°C for 10 min and immediately put on ice. The RNA was loaded and electrophoresis was performed at 5 V/cm until the bromophenol blue band had migrated two thirds of the length of the gel. The gel was photographed and washed for 10 min in H_2O to remove formaldehyde.

The RNA was transferred from the gel to Hybond N+ membrane (Amersham) by capillary transfer (Sambrook *et al.*, 1989) overnight using 20 x SSC (3 M NaCl, 0.3 M sodium citrate, pH 7.0) as transfer buffer.

The membrane was shortly washed with 2 x SSC and baked between Whatman 3MM filter paper for 30 min at 120°C.

Hybridization and detection

The RNA was detected using the DIG system (Boehringer Mannheim).

Labeling of the DNA probe:

Primers specific for the *dsbA* homolog of strain Z2491

(forward primer: 5'-GCTTTGACTTCATTGACCCTGTTGGCATTGGCC; (SEQ ID N°97)

reverse primer: 5'-TATCCACCAACTGGTCAATCGTGGTCATACCGG) SEQ ID N°98 were used in PCR amplification with DIG-labeled dUTP. Template chromosomal DNA of strain Z2491 was isolated as described (Sarkari *et al.*, 1994). The PCR reaction mixture contained template DNA (1 µg/ml); reaction buffer (10 mM Tris-Cl, pH 8.0, 50 mM KCl, 1.5 mM $MgCl_2$, 0.01% gelatin); PCR DIG probe synthesis mix (200 µM dATP, dCTP, dGTP each, 190 µM dTTP, 10 µM digoxigenin-11-dUTP; Boehringer); forward and reverse primer (100 nM each) and Taq polymerase. The PCR reaction was incubated 1 min at 94°C, followed by 30 cycles of 1 min at 94°C, 1.5 min at 60°C and 2 min at 72°C followed by incubation for 5 min at 72°C. The labeled PCR product was purified using the Qiaquick PCR Purification Kit (Qiagen).

Hybridization conditions:

For prehybridization, the membrane was incubated for 2 h at 42°C with 20 ml of hybridization solution (High SDS Buffer: 7% SDS, 50% formamide, 5 x SSC, 2% Blocking Reagent (Boehringer), 50 mM sodium-phosphate, pH 7.0, 0.1% N-lauroylsarcosine) in a hybridization tube. This solution was replaced by 10 ml hybridization solution containing 250 ng of labeled probe. For denaturation, this solution was heated at 68°C for 10 min before adding. Hybridization was performed overnight at 42°C. After that, the membrane was washed 2 x 5 min at room temperature with 2 x SSC, 0.1% SDS and 2 x 30 min at 68°C with 0.5 x SSC, 0.1% SDS.

Detection by chemiluminescence:

After hybridization and washing, the membrane was equilibrated for 1 min in maleic acid buffer (100 mM maleic acid, 150 mM NaCl, pH 7.5). The membrane was blocked by gentle agitation in blocking solution (1% Blocking Reagent (Boehringer) in maleic acid buffer), followed by incubation with antibody solution (Anti-Digoxigenin, Fab fragments conjugated to alkaline phosphatase, 1:10000 in blocking solution) for further 30 min. The membrane was washed 2 x 15 min with maleic acid buffer and then equilibrated for 2 min in detection buffer (100 mM Tris-Cl, 100 mM NaCl, pH 9.5). The chemiluminescence substrate CSPD was diluted 1:100 in detection buffer. The membrane was treated with CSPD-solution for 5 min at room temperature in a sealed bag. After removing the CSPD-solution, the membrane was sealed again and incubated for 15 min at 37°C. The membrane was exposed to X-ray film for 1 h.

II. Creation of an isogenic DsbA mutant of meningococci

Oligonucleotides were designed to amplify DNA fragments extending about 1 kilobase on either side of the first cysteine codon in *dsbA* (SEQ ID N°1) (This cysteine is immediately after the predicted site of proteolytic cleavage in the maturation of the protein DsbA). Oligonucleotides were designed such that a ligation of the two fragments recreates the DNA sequence of DsbA and some flanking sequence, with the exception that there is an

*Eco*RI restriction endonuclease site (an *Eco*RI site) in place of the DNA sequence coding for the predicted protease recognition site, the first cysteine codon is no longer present, there is an in-frame translational stop codon and the transational frame of the rest (3') of the gene is shifted by one base.

Oligonucleotides used to amplify the 5' end of the DsbA gene plus upstream sequence were:

b31331: GAACATGGATCCCGTCCACACACTTTACG
(SEQ ID N°91)

b31311: GCGGCCGAATTCCAACAGGGTCAATGAAGT
(SEQ ID N°92)

Oligonucleotides used to amplify the 3' end of DsbA plus downstream sequence were

b31312: CTGTTGGAATTCGGCCGCTTGTAGCAAACAGGCT
(SEQ ID N°93)

b31313: TAGTACGGTACCGATTCACTTGGTGCTT
(SEQ ID N°94)

In order to mutate the *dsbA* gene PCR amplification was performed using chromosomal DNA from strain 8013 (a serogroup C clinical isolate) as template.

Oligonucleotides b31311 and b31312 contain complementary sequences, such that mixture of the two PCR products in the presence of the two 'external' oligonucleotides b31331 and b31313 results in 'PCR ligation' forming the DNA fragment extending from the position of b31331 to that of b31313, and including the modifications described above. This fragment was cleaved with the enzymes *Bam*HI and *Kpn*I and cloned into appropriately cleaved vector pBluescript II SK(+), which was then propagated in *E. coli* DH5α. This construction was linearised by digestion with *Eco*RI. Into the *Eco*RI site was inserted a resistance cassette containing a gene encoding resistance to erythromycin and two neisserial uptake sequences (GCCGTCTGAA) which have been shown to be necessary for efficient transformation of Nm [Goodman, S. D., and Scocca, J. J. (1988).

Identification and arrangement of the DNA sequence recognized in specific transformation of *Neisseria gonorrhoeae*. *Proc. Natl. Acad. Sci. USA 85*, 6982-6986]. The plasmid containing the *dsbA* gene interrupted by the erythomycin resistance cassette was used to transform Nm to erythromycin resistance, selecting on 2 µg/ml erythromycin. Chromosomal DNA, prepared from a selected transformant strain was used to back transform the parental strain 8013 (serogroup C ; see Nassif X., D. Puaoi, and M. So. Transposition of Tn1545-*3 in the pathogenic Neisseriae: a genetic tool for mutagenesis, Journal of Bacteriology, 1991, 173, 2147-2154) and several hundred transformant colonies were taken to give a statistically homogeneous genetic background.

The transformant strain was tested by western blot in order to show that it no longer expressed the protein DsbA, using either rabbit anti-whole cell (strain Z5463) or anti-DsbA antiserum.

The overall strategy is illustrated by figure 46 which shows the production of a knockout mutation of DsbA. On this figure, ORF are shown as arrows (note that the sequence shown is that of Z2491 and that strain 8013 does not contain the ORF *rei*1 ; the PCR product b31331-31311 is correspondingly shorter). The position of the oligonucleotide primers are shown as small arrows. PCR products are shown as shaded boxes. The two PCR products were ligated (fig. 46a) and cloned into the vector pBluescript. After linearisation of the plasmid by cleavage with *Eco*RI, the resistance cassette (dark grey) was inserted (fig. 46b). This construction was used to transform Nm to erythromycin resistance (fig. 46c), thus replacing the wild-type *dsbA* gene with that interrupted with the resistance cassette.

III. Cloning and expression of DsbA for use in production of anti-DsbA antiserum

Overview of cloning strategy. The antigen DsbA is predicted to be a lipoprotein, whose lipophilic signal sequence is cleaved to leave an N-terminal cysteine residue which is subsequently modified by the addition of (a) fatty acid molecule(s) for anchorage in the

outer membrane [Pugsley, A. P. (1993). The complete general secretory pathway in Gram-negative bacteria. *Microbiol. Rev. 57*, 50-108]. This signal sequence is not present in the mature protein. After cloning and overexpression of the gene, if the protein were exported in large quantities to the outer membrane of the host *E. coli* it could prove toxic for the bacteria. On the basis of these considerations, the gene was not cloned in its entirety, but only the sequence coding for the predicted mature protein was cloned and expressed. In order to minimise the metabolic load on the host bacteria, the (codon for the) N-terminal cysteine of the mature protein was replaced by a (codon for a) serine.

Primers were designed in order to amplify DNA corresponding to the predicted mature protein DsbA and to allow subsequent ligation into an expression vector which links the protein at its C-terminal end to a hexahistidine tract (His-tag) in order to facilitate subsequent purification, using a nickel affinity column.

Oligonucleotides
b31316b (GCTTGTGGTACCATATGAGCAAACAGGCTGAAACCAGT ;
SEQ ID N°95)
and b31317 (TCAATCCTCGAGTTGCGGCTTTTTCTGCTCTT ;
SEQ ID N°96) were designed to amplify a fragment from the chromosome of Nm strain Z2491. Oligonucleotide b31316b contains a recognition site for the restriction endonuclease *Nde*I (CATATG) allowing the fragment to be cloned into the expression vector pET20b(+) (Novagen R&D systems). The latter half of this site specifies the amino acid methionine, which is the N-terminal amino acid of the expressed protein. This is followed by a codon specifying serine (which was chosen to replace the N-terminal cysteine of the mature protein) and subsequently by bases corresponding to the gene sequence. The oligonucleotide b31317 causes the replacement of the gene's natural stop codon with the first three bases of an *Xho*I site (CTCGAG), which allows an in frame link to the expression vector's hexahistidine encoding sequence. Translation is terminated after the hexahistidine by a stop codon in the vector.

Overview of strategy for overexpression of the cloned protein. The expression vector takes advantage of an *Nde*I site to allow insertion of a coding DNA sequence such that the second half of this site (ATG) is recognised by the ribosome as the first amino acid of the recombinant protein to be expressed. Since cleavage by the enzyme *Nde*I is particularly inefficient near the extremity of a PCR product, it is easier to clone the PCR product using another method (either using a site incorporated into the oligonucleotide 5' to the *Nde*I site, by 'TA cloning', or by enzymatically blunting the fragment and ligating into a 'blunt-ended' restriction ezyme site) then excise the coding fragment using the enzymes *Nde*I and that at the 3' end of the gene). This fragment is then ligated into the expression vector and the resulting plasmid grown in *E. coli* strain DH5α, which is highly transformable and will not be harmed by the expression of the potentially toxic foreign protein since it is incapable of initiating transcription from the T7 RNA polymerase promoter in the expression vectors. Plasmid isolated from DH5α is then used to transform (at high efficiency) *E. coli* strain BL21(DE3). This strain contains a gene for T7 RNA polymerase preceded by the *lac* promoter and hence inducible by isopropyl b-D-thiogalactoside (IPTG). Addition of IPTG to the culture medium induces the transcription of the T7 RNA polymerase gene. The recombinant protein gene is read by the T7 RNA polymerase, and the transcript translated to overproduce the recombinant protein.

Cloning of the DsbA gene. The PCR products from b31316b and b31317 using chromosomal DNA as template were blunted (using the Klenow fragment of *E. coli* DNA polymerase and T4 phage polynucleotide kinase in the presence of the four deoxynucleotide triphosphates and ATP) and ligated into the *Sma*I site of plasmid pUC18. The ligation mixtures were used to transform *E. coli* DH5α, and the resulting plasmid were cleaved with *Nde*I and*Xho*I. The liberated fragment was gel purified and ligated into the expression vector pET-20b(+). The ligation mixture was used to transform *E. coli* DH5α, then plasmid was isolated and used to transform BL21(DE3). Individual colony isolates were screened for production of the recombinant protein by SDS-PAGE. One

isolate was chosen for subsequent use in protein purification. This isolate was designated 2g:

Name	*E. coli* strain	construction	expressed protein
2g	BL21(DE3)	pET20b(+):PCR product b31316b-b31317	DsbA-(C-terminal his tag)

Purification of the recombinant proteins. Recombinant DsbA protein was purified using an affinity column produced with Poly-His protein purification resin. Bacteria (20 to 50 isolated colonies of overnight growth on LB agar containing 100 mg/ml of ampicillin) were inoculated into 500 ml of LB medium containing 100 mg/ml of ampicillin and incubated at 37°C in a conical flask with orbital shaking to maintain aeration. When the OD at 600 nm of the culture had reached between 0.4 and 0.5, the expression of the protein was induced by addition of IPTG to 2 mM. Growth was continued for a further 2 hours, then the bacteria were harvested by centrifugation at 3500 x g for 25 minutes. The pellets were sonicted (three times 5 minutes, on ice) in 10 ml of PBS to break the cells. The suspension was centrifuged at 15000 x g and the supernatant taken. For purification, 5 ml of the supernatant was passed through a column made from 1 ml of 'poly-His protein purification resin' (Boehringer Mannheim). The column was washed with 5 ml of PBS containing 10 mM imidazole, then 5 ml of PBS/20 mM imidazole. The recombinant DsbA protein was eluted in PBS/50 mM imidazole, then PBS/500 mM imidazole. Fractions containing pure recombinant DsbA (by SDS-PAGE analysis) were pooled and dialysed against PBS. Stocks containing recombinant DsbA at 100 µg/ml were stored at -80°C.

IV. Immunisation of a rabbit with recombinant DsbA.

New Zealand white rabbits were immunised three times at intervals of 15 days with 100 µg of recombinant DsbA (preparation 2g).

1st immunisation 2 ml of antigen '2g' in PBS:Freund's complete adjuvant (1:1)

2nd immunisation 2 ml of antigen '2g' in PBS:Freund's incomplete adjuvant

(1:1)

3rd immunisation 2 ml of antigen '2g' in PBS:Freund's incomplete adjuvant (1:1)

Blood was taken from the rabbits 3 weeks after the third immunisation and allowed to clot overnight. Serum was separated from the clot by centrifugation and stored in aliquots at -80C.

V. Immunofluorescence staining of meningococci

Meningococci were grown for 18 hours on GCB-agar (Difco), then resuspended in PBS. Drops of suspension were immediately placed on glass microscope slides and allowed to dry at 45°C. The bacteria were fixed to the slide by adding methanol and allowing to evaporate (twice). The bacteria were pretreated with PBS containing 1% gelatin, then reacted with the primary antibody (1/1000 dilution of the rabbit anti-recombinant DsbA in PBS/gelatin) for 30 minutes at room temperature. The slides were washed twice for 2 minutes in an excess of PBS, then reacted with 1/200 dilutions the secondary antibody in PBS/gelatin (sheep anti-rabbit immunoglobulin G-Cy3-conjugate) for 30 minutes at room temperature. Slides were washed three times for 5 minutes in an excess of PBS, then the bacteria were counterstained with DAPI (1 µg/ml in PBS/10% methanol) and rinced twice in PBS. The slides were allowed nearly to dry, then the mounting fluid 'morviol' (Sigma) was added to the bacteria and cover slips were fixed in place. The bacteria and fixed antibodies were visualised by ultraviolet and light microscopy.

Anti-DsbA antiserum gave a halo of reacting antibodies around the wild type Nm (8013) which was reduced to the background level of reactivity of the secondary (sheep anti-rabbit immunoglobulin G) antibody alone in the case of the DsbA mutant. These results are illustrated by figures 47A and 47B, which show an immunofluorescence microscopy of wild-type and DsbA mutant bacteria with anti-recombinant DsbA antiserum: figure 47A, wild-type Nm 8013 reacted with anti-DsbA antiserum and revealed with anti-rabbit immunoglobulin G-Cy3 conjugate ; figure 47B, DsbA mutant 8013 reacted with anti-DsbA antiserum and revealed with anti-rabbit immunoglobulin G-Cy3 conjugate.

This demonstrates that the DsbA protein is exposed at the surface of the bacteria.

V. Assay for the bactericidal activity of the rabbit anti-recombinant DsbA antiserum

Volumes of 10 µl of PBS containing 2000 bacteria were mixed with 500 µl of freshly-thawed rabbit serum. Volumes of 95 µl were taken from the assays for enumeration imediately and at time points up to 90 minutes after addition of the serum. Enumeration was performed by plating 50 µl aliqots of 10-fold dilutions of the assays onto GCB agar (Difco).

The results show that while the antiserum killed 65% of the parental meningococcus (strain 8013) within 20 minutes and all of the bacteria within 60 minutes, the preimmune serum (serum taken from the rabbit before the first immunisation) killed none after 20 minutes and only half after 60 minutes. Hence the antiserum is capable of killing heterologous meningococci (The DsbA sequence was taken from strain Z2491). This is illustrated by figure 48 which shows the bactericidal activity of anti-DsbA and the corresponding preimmune antiserum.

The bactericidal activity of the antiserum against the parental strain 8013 was compared with that against the isogenic mutant containing an interrupted DsbA gene (and shown by western blot not to express this protein). In this case freshly-thawed anti-recombinant DsbA antiserum was added to the parental and to the DsbA mutant. The results show that the bactericidal activity is specific for the DsbA-expressing strain, since the parental strain was killed to a much greater extent than was the mutant. This is illustrated by figure 49, which shows the bactericidal activity of anti-DsbA antiserum against meningococci expressing an isogenic mutant lacking the protein DsbA.

SEQUENCE LISTING BRIEF SUMMARY

SEQ ID N°	Sequence nature	Nm strain source	product name
			DsbA Allele 1
1	nucleotides	Z2491	*dsbA*
2	aminoacids	Z2491	DsbA
3	nucleotides	Z3524	*dsbA*
4	aminoacids	Z3524	DsbA
5	nucleotides	Z3842	*dsbA*
6	aminoacids	Z3842	DsbA
7	nucleotides	Z4667	*dsbA*
8	aminoacids	Z4667	DsbA
9	nucleotides	Z4707	*dsbA*
10	aminoacids	Z4707	DsbA
11	nucleotides	Z5005	*dsbA*

12	aminoacids	Z5005	DsbA
13	nucleotides	Z6466	*dsbA*
14	aminoacids	Z6466	DsbA
15	nucleotides	Z7176	*dsbA*
16	aminoacids	Z7176	DsbA
			DsbA Allele 2
17	nucleotides	Z4662	*dsbA*
18	aminoacids	Z4662	DsbA
19	nucleotides	Z6904	*dsbA*
20	aminoacids	Z6904	Dsba
			DsbA Allele 3
21	nucleotides	Z4259	*dsbA*
22	aminoacids	Z4259	DsbA
23	nucleotides	Z4673	*dsbA*

24	aminoacids	Z4673	DsbA	
				DsbA Allele 4
25	nucleotides	Z4683	*dsbA*	
26	aminoacids	Z4683	DsbA	
				FhaB
27	nucleotides (3' end 1047 ones)	Z2491	*fhaB*	
28	aminoacids	Z2491	FhaB	
				FhuA
29	nucleotides	Z2491	*fhuA*	
30	aminoacids	Z2491	FhuA	
31	nucleotides	Z3524	*fhuA*	
32	aminoacids	Z3524	FhuA	
33	nucleotides	Z3842	*fhuA*	
34	aminoacids	Z3842	FhuA	
35	nucleotides	Z4259	*fhuA*	
36	aminoacids	Z4259	FhuA	

37	nucleotides	Z4662	*fhuA*
38	aminoacids	Z4662	FhuA
39	nucleotides	Z4667	*fhuA*
40	aminoacids	Z4667	FhuA
41	nucleotides	Z4673	*fhuA*
42	aminoacids	Z4673	FhuA
43	nucleotides	Z4683	*fhuA*
44	aminoacids	Z4683	FhuA
45	nucleotides	Z4707	*fhuA*
46	aminoacids	Z4707	FhuA
47	nucleotides	Z5005	*fhuA*
48	aminoacids	Z5005	FhuA
49	nucleotides	Z6904	*fhuA*
50	aminoacids	Z6904	FhuA

51	nucleotides	Z7176	*fhuA*	
52	aminoacids	Z7176	FhuA	
				Rni5
53	nucleotides	Z2491	*rni5*	
54	aminoacids	Z2491	Rni5	
				Rth17 à 21
55	nucleotides	Z2491	*Rth17*	
56	aminoacids	Z2491	Rth17	
57	nucleotides	Z2491	*rth18*	
58	aminoacids	Z2491	Rth18	
59	nucleotides	Z2491	*rth19*	
60	aminoacids	Z2491	Rth19	
61	nucleotides	Z2491	*rth20*	
62	aminoacids	Z2491	Rth20	
63	nucleotides	Z2491	*rth21*	
64	aminoacids	Z2491	Rth21	

TolC Allele 1				
65	nucleotides	Z2491	*tolC*	
66	aminoacids	Z2491	TolC	
67	nucleotides	Z3524	*tolC*	
68	aminoacids	Z3524	TolC	
TolC Allele 2				
69	nucleotides	Z4707	*tolC*	
70	aminoacids	Z4707	TolC	
TolC Allele 3				
71	nucleotides	Z3842	*tolC*	
72	aminoacids	Z3842	TolC	
73	nucleotides	Z4259	*tolC*	
74	aminoacids	Z4259	TolC	
75	nucleotides	Z4662	*tolC*	

76	aminoacids	Z4662	TolC
77	nucleotides	Z4667	*tolC*
78	aminoacids	Z4667	TolC
79	nucleotides	Z4673	*tolC*
80	aminoacids	Z4673	TolC
81	nucleotides	Z4683	*tolC*
82	aminoacids	Z4683	TolC
83	nucleotides	Z5005	*tolC*
84	aminoacids	Z5005	TolC
85	nucleotides	Z6466	*tolC*
86	aminoacids	Z6466	TolC
87	nucleotides	Z6904	*tolC*
88	aminoacids	Z6904	TolC
89	nucleotides	Z7176	*tolC*
90	aminoacids	Z7176	TolC

				PCR oligo
91	nucleotidic forward primer	Z2491	*dsb*A 5' end	***dsb*A**
92	nucleotidic reverse primer	Z2491	*dsb*A 5' end	

93	nucleotidic forward primer	Z2491	*dsb*A 3' end	
94	nucleotidic reverse primer	Z2491	*dsb*A 3' end	
95	nucleotidic forward primer	Z2491	dsbA 5' end	
96	nucleotidic reverse primer	Z2491	dsbA 3' end	
Primers				
97	nucleotidic forward primer	Z2491	*dsb*A	***dsb*A**
98	nucleotidic reverse primer	Z2491	*dsb*A	
99	nucleotidic forward primer	Z2491	*fhu*A	***fhu*A**
100	nucleotidic reverse primer	Z2491	*fhu*A	
101	nucleotidic forward primer	Z2491	*rni*5	***rni*5**
102	nucleotidic reverse primer	Z2491	*rni*5	
103	nucleotidic forward primer	Z2491	*tol*C	***tol*C**
104	nucleotidic reverse primer	Z2491	*tol*C	
105	nucleotidic forward primer	Z2491	*rth*17	***rth*17**
106	nucleotidic	Z2491	*rth*17	

	reverse primer			
107	nucleotidic forward primer	Z2491	*rth*18	***rth*18**
108	nucleotidic reverse primer	Z2491	*rth*18	
109	nucleotidic forward primer	Z2491	*rth*19	***rth*19**
110	nucleotidic reverse primer	Z2491	*rth*19	
111	nucleotidic forward primer	Z2491	*rth*20	***rth*20**
112	nucleotidic reverse primer	Z2491	*rth*20	
113	nucleotidic forward primer	Z2491	*rth*21	***rth*21**
114	nucleotidic reverse primer	Z2491	*rth*21	
115	nucleotidic forward primer	Z2491	*fha*B	***fha*B**
116	nucleotidic reverse primer	Z2491	*fha*B	